AC140889 Homo sapi AC067900 Homo sapi AC073487 Homo sapi

AC025406 Homo sapi

AC024384 Homo sapi AC024384 Homo sapi AL450325 Human DNA

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Sequence:

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Searched:

Database

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Hominidae; Homo.

15. (Dases 1 to 4069)

16. Tarpeira, P., Ruiters, M.H.C., de Leij, L.F.M.H. and Harmsen, M.C.
Terpeira, P., Ruiters, M.H.C., de Leij, L.F.M.H. and Harmsen, M.C.
Terpeira, P., Ruiters, M.H.C., de Leij, L.F.M.H. and Harmsen, M.C.
Use of the EGP-2 promoter for targeted expression of heterologous genes in carcinoma-derived cell lines

L. Unpublished

M.C. Unpublished

M.C. Arzpis, M., Kroesen, B.-J., Helfrich, W.,
Terpeira, P., Ruiters, M.H.C., de Leij, L.F.M.H. and Harmsen, M.C.
Direct Submission

L. Submitted (04-28P-2002) Path-LabMed-Mol-Biol University Groningen, Hanzeplein 1, Groningen 971362, The Netherlands

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AX148099 4069 bp DNA linear PRI 12-NOV-2002
Homo sapiens EGP2 (TACSTD1) gene, promoter region and 5'UTR.
AX148099
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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/product="BGP2"
/note="putative transcription start"
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/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
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AL450325
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AC1420898
AC105135
AC10510
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AUTHORS
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JOURNAL
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AL451053 Homo sapi
AL590133 Human DNA
AC117378 Homo sapi
AL137003 Human DNA
AC003663 Homo sapi
AC067818 Homo sapi
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AC008627 Homo sapi
AL121583 Human DNA
AC017079 Homo sapi
AL137852 Human DNA
BD152002 Primer fo
AX871940 Sequence
AX871940 Sequence
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(without alignments)
8453.521 Million cell updates/sec
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                    GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                           5883141 segs, 28421725653 residues
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359
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AC117378
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Gapop 10.0 , Gapext 1.0
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AC079775 171987 bp DNA linear PRI 21-APR-2005
Homo sapiens BAC clone RP11-295P2 from 2, complete sequence.
AC079775
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3308 GCGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTCTTACATCTTCAAGTGCTAGAAAT 3367
                                                      3368 GCTTATGAAAAACGAAAAAAGAATTATTAAGAGTAATTATAAAGAAACACTCATTTTCTTC 3427
                                                                                                                                               Louis,
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                                    240
                                                                                                            3488 AGGAGTATAATTAAAATTGCCAGGTAAAAGCTCAAAGGTCTTTTTTATAAGTGTTCTGGAA 3546
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-MAY-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, 5 (bases 1 to 171987)
                                    Submitted (30-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (10-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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University School of Medicine, 4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae, Howo.

1 (bases 1 to 171987)

Elliott, G., Doebber, A., Belter, B. and Haakenson, W. The sequence of Homo sapiens BAC clone RP11-295P2 (Unpublished (2001)

2 (Does 1 to 171987)

Waterston, R.H.
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On Mar 30, 2002 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
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Waterston, R.H.
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4 (bases 1 to 171987)
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Non-squamous epithelium-specific transcription
Patent: WO 0171015-A 5 27-SEP-2001;
Rijksuniversiteit Groningen (NL)
Location/Qualifiers
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                          Score 359; DB 8;
Pred. No. 9.6e-69;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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     /gene="TACSTD1"
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Homo sapiens
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Submitted (06-07-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (Dases 1 to 56173)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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DOE Joint Genome Institute and Stanford Human Genome Center.
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100.0%; Pred. No. 8.4e-69;
tive 0; Mismatches 0;
                                                                                            /product="unknown"
/protein_id="AAY15096.1"
/db_xref="G1:62822548"
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DOE Joint Genome Institute.
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join(64495. .64570,68452. .68559,68797. .69037,70223. .70288,72003. .72066,73942. .74043,74758. .74958,80155. .80199,
                                                                                                                                                                                                                                                                                                                                                                               NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-261E8; the clone sequenced to the right is RP11-436K12. Actual start of this clone is at base position 1 of RP11-295P2; actual end is at base position 171987 of RP11-295P2.
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/db_xref="G1:6382547"
/translation="MAPPOVLAFGLILAAATATFAAAQEECVCENYKLAVNCFVNNNR
OCOCTSVGAQNTVICSKLAAKCLYMKAENNGSKLGRRAKFEGALQNNDGLYDPOCDES
GLFKAKQCNGTSMCWCVNTAGVRRTDKDTEITCSERVRTYWIIIELKHKAREKPYDSK
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DVKGESLFHSKKMDLIVNGEQLDLDPGQTLIYYVDEKAPEFSMQGLKAGVIAVIVVVV
IAVVAGIVVLVISRKKRMAKYEKAEIKEMGEMHRELNA"
                                        Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
                                                                                                                                                                             The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
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/gene="Homo sapiens tumor-associated calcium signal
transducer 1 (TACSTD1), mRNA.; H NH0295P02.1
trans gene was based on g1(4505058)"
/codon_start=1
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107403. .107549,109258. .109407,111285. .111418,
124731. .124930,140537. .140646,158020. .158143,
161647. .161797,165954. .166051)
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107403. .107549,109258. .109407,111285. .111418,
124731. .124930,140537. .140646,158020. .158143,
161647. .161797,165954. .>166051)
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64313. .82007
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/note="CpG island (*GC=67.1, o/e=0.92, #CpGs=76)"
99113. .166051
/gene="MSH2"
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/db_xref="taxon:9606"
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/clone_lib="RPCI-11"
64058. .65106
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/gene="TACSTD1"
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                                      MAPPING INFORMATION: Mapping information
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join(<9622. .9747,11016. .11216,36537. .36690,38920. .38961,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
        Submitted (26-JAN-2002) DOE Joint Genome Institute, 2800 Mitchell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (17-JUN-1999) Bender E., Functional Genomics, Janssen Pharmaceutica, Turnhoutseweg 30, B-2340 Beerse, BELGIUM Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CCCGCCTAATTTTGTATCTTTTAGTAGAGACGCGTTCCTCCATGTTGGTCAGGCTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                           Drive, Walnut Creek, CA 94599, USA
On Jan 26, 2002 this sequence version replaced gi:7710540.
Draft Sequence Produced by DOB Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
Waw-sing.cstanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
                                                                                                                                                                                                                                                                                                                                                                        37.0%; Score 132.8; DB 8; Length 56173; 76.8%; Pred. No. 4.2e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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ches 52;
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5-HT4 gene; 5-HT4 receptor.
Homo sapiens (human)
Homo sapiens
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Direct Submission
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Matches 175; Conserv
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Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requester: clonerequest@sanger.ac.uk cn Jai, 2000 this sequence version replaced gi:9230894.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw.; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20 RPI1-358N2 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. Por further details see
150477 TCGAACTTCTGACCTCAGGTGATCCGCCCCCCCTCGGCCTCCCCAAGTGCTGGGATTACAG 150418
                                                                                                                                                                                                                                    150417 GCATGAGCCACCGCCCGGCCAGGAATGAGGTTTTGATACATGCTACCACATGGATGAA 150358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSBA358N2 84710 bp DNA linear PRI 18-MAY-2005 Human DNA sequence from clone RP11-358N2 on chromosome 20 Contains the 5' end of the ASXL1 gene for additional sex combs like 1 (Drosophila) and a CpG island, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
                                                                                                                                                                                    121 GCGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTCTTACATCTTCAAGTGCTAGAAAT 180
                                                                                TCGAACTTCAAACCTCAGGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTAGGATTACAG 120
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
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AL121583.25 GI:9588417
HTG; ASXL1; CpG island; KIAA0978.
Homo sapiens (human)
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Pinishing Completed at Stanford Human Genome Center
Www.shgc.stanford.edu
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www.shgc.stanford.edu
Batimated Total Number of Errors is 0.
Bothing insert is not the entire sequence of the clone (entire sequence is 197.3kb). It is clipped at the overlap with ACO11390.
The number of bases overlapped is 138359.
Location/Qualifiers
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DOB Joint Genome Institute and Stanford Human Genome Center.
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Submitted (11-APR-2002) DOB Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Apr 11, 2002 this sequence version replaced gi:12830083.
Draft Sequence Produced by DOB Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 15353)
DOG Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
Unpublished
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                                                                   Length 130985;
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                                                             Score 132.8; DB 8;
Pred. No. 4e-19;
0; Mismatches 52;
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/db_xref="taxon:9606"
/chromosome="5"
/clone="CTB-160022"
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DOE Joint Genome Institute.
Direct Submission
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                                                                   37.0%;
76.8%;
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Homo sapiens
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Matches 175, Conservative
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/translation="MCVVNFFRASEDLOYLENYSDAPMTPKQILQVIEAEGLKEMRS GTSPLACLNAMLHSNSRGGEGLFYKLPGRISLFTLKV"
join(15768. 15850,17111. 17113,18399. 18507,77512. 77806,78722. 79304)
/gene="ASXL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         locua_tag="RPI1-358N2.1-004"
|oin(15768. .15850,17111. .17113,18399. .18507,77512. .77806,
|8722. .79304|
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.21553)
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                   /locus tag="RP11-358N2.1-002"
/note="match: ESTs: AI034028.1 AI829840.1 BM929970.1
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Homo sapiens BAC clone RP11-462M9 from 2, complete sequence.
AC017079
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|standard_name="OTTHUMP000000030593"
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/note="Clone_left_end: RP5-1184F4"
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8
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/protein_id="CA140415.1"
/bx.ref="G1:57162102"
/db_xref="G1:57162102"
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/note="match: ESTs: BM906623.1"
21913. .21918
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                                                                                                                                                             join(7<u>9</u>02_ .8216,15768. .15850,17111. .17113,18399. .18507,77512. .77632,77709. .77806,78722. .78815,79285. .79437,80705. .80868,80967. .81063,82264. .82369,82668. .83301,83816. .84710,AL034550.31:101. .4093)
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21548. .21937}
        .18507,
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?1548. .21614)
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join(8999. .9175,15768. .15850,17111. .17113,18399. .18507,
21548. .21937)
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GOMEWTGVMLPRRVVLFTEKNVAHVEBASGFSGGHADGESGSPSSSSGSLALGSAAIR
GOABVTQDPAPLLRGFRKPATGGMKRNRGEEIDFETFGSILVNTNLRALINSRTFHAL
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SLPQETVDGEPROGKESPEAAASAS PPERKRELEDROSPRATIESVHTEKPOPTKEE
PKVPPIRIOLSRIKPRKNSEQPAYOJCPRII PTTESSCRGWTGARTLADIKARALOV
RGARGHHCHREAATTAIGGGGGPGGGGGGATDEGGGRGSSGDGGEACGHPEPRGGPS
PRGCTSBLORTQLLPPYPLNGHTTQAATAMSRARBDLPSIRRESCELQARTVGLT
DGLGDASQLPWPLARPYPLNGHTTQAATAMSRARBDLPSIRRESCELQARTVGLT
DGLGDASQLPWPATGGCOOLDLSSQTSVARRLVEDPOPLOATSWES
DDEGGGPTVPADNGPILSLSSQTSVARRLVEDPOLAFPSTSWES
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SREHIPSVEPQVGEEWEKAAPTPPALPGDLTAEEGLDPLDSLTSLWTVPSRGGSDSNG
SYCQQVDIEKLKINGDSEALSPHGESTDTASDFEGHLTEDSSEADTREAAVTKGSSVD
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KANAENRKATGHSPLELVGHLEGMPFVMDLPFWKLPREPGKGLSBPLEPSSLPSQLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(8195. .8216,15768. .15850,17111. .17113,18399. .18507,
21548. .21614)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSHFQQQLLFLLPEVDRQVGTDGLLRLSSSALNNEFFTHAAQSWRERLADGEFTHEMQ
VRI RQEMEKEKKVEQWKEKFFEDYYGQKLGLTKEESLQQNVGQEEAEIKSGLCVPGES
VRI QRGPATRQRDGHFKKRSRPDLRTRARRNLYKKQESEQAGVAKDAKSVASDVPLYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRAVCLSMPGSSVEATNPLVMQLLQGSLPLEKVLPPAHDDSMSESPQVPLTKDQSHGS
LRMGSLHGLGKNSGMVDGSSPSSLRALKEPLLPDSCETGTGLARIEATQAPGAPQKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAVPSFDSLHPVTNPI TSSRKLEEMDSKEQFSSFSCEDQKEVRAMSQDSNSNAAPGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGDLTTSRTPRFSSPNVISFGPEQTGRALGDQSNVTGQGKKLFGSGNVAATLQRPRPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KQAFYGKLSKLQLSSTSFNYSSSSPTFPKGLAGSVVQLSHKANFGASHSASLSL<u>O</u>MFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDEKPNWNQSAPLSKVNGDMRLVTRTDGMVAPQSWVSRVCAVRQKIPDSLLLASTEYQ
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BE952301.1 BF848475.1 B1094451.1 BM456370.1 BM676077.1
BM985410.1 BM988291.1 BM991942.1 BQ066322.1 BQ064719.1
BM985410.1 BM988291.1 BM951242.1 BQ08559.1 BU686340.1
CA313728.1 CA417500.1 CA417510.1
match: cDNAs: AB023195.2 AJ438952.1 AK025756.1 AL117518.1
join(7902. .8216,15768. .15850,17111. .17113,18399. .185
77512. .77632,77709. .77806,78722. .78815,79285. .79437,
80705. .80868,80967. .81063,82264. .82369,82668. .83301,
83816. .84710,AL034550.31:101. .4093)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSSTVESISLQCACSLKAMIMCQGCGAFCHDDCIGPSKLCVLCLVVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard_name="OTTHUMP00000030592"
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                                                                                                                                   /locus tag="RP11-358N2.1-001"
join(7902. .8216,15768. .1585
                                                                                                                                                                                                                                                                               /gene="ASXL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL117647.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
        gene
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ALOTOTORNAKNETTKWAKEGARALAGADIAESUNGALATINGFALE JIEN JIEN JIEN JULUTOTORNAKNETTKWAKEGARALAGADIAESUNGALGATINGFALE JIEN JIEN JULUTOTORNAKNETTKWAKEGARALAGADIAESUNGALGANGKESESKWDFI LISHAVYCRUVLKKKGGRAVISNGRIIGPLEDSELFNODPHILLENIILKRYSGCKIKG HIQOHAVCRUVLKUREDVEDVAKUADALYKURDENISORKIKGHINGAREDHANGAREGETYFDV HIQOHARAGARALAGANGADALINMULKYFMNCGSKLSDMPLKSFYRYULEPEISF TSDNSPAKGPTAKILAEGATSANPYUTUTIVMAHAUGYFGANPADSANBEYSTALEGANPOSTANPATALAGAGANPANDELL SUGTSSANPYUTUTIVMAHAGYFGANPOSTANPATALAGANPANDELL SUGTSSANPSTRYPETUNTIVMAHAGYFGANPADSAN KNYKTPVKKPTKNYLSPFTENIPTANPSTRYPETUNTYKYPKKATKANAPANDELL SUGTSSANBSGRWDSFKWGFTGGKTEEVKQDKDDIINIFSVASKIIKVKVÇKKADWYNBDLL SUGTSSANBSGRWDSYNWYELFUDVRPPLVDKFFFINMAHAGYTEGRINGOT VKILFLDULPPLVUDKFLFVDADAQIVRTDLKGELRDFNLDGAPYGYTPPFCDSRRENDGY KNIKTPVKKFTKNISALYVDDLKKFRKIAAGDRLAGGYGGLSQDPNSLSNLDG DLANNAHHOVPI KSLPGEMLACETWODDASKKRAKTITDLCNNPWTKEPKLBAAVRIVP EWQDYDQIINGARCHTSALYVDDLKKFRKIAAGDRLAGGYGGLSQDPNSLSNLDG DLANNAHHOVPI KSLPGEMLACETWODDASKKRAKTITDLCNNPWTKEPKLBAAVRIVP EWQDYDGIISLAGK (** #CPGS=19)" | 65966 | . 54786 | . 67196 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 | . 61906 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(2003...2101,2906. .2929,3766. .3860,6028. .6234,
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17719. .17798,19087. .19276,20295. .20453,721287 .21372,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="NFFVDDYARFTILDSQGKTAAVANSMNYLTKKGMSSKEIYDDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRPVTFWIVGDFDSPSGRQLLYDAIKHOKSSNNVRISMINNPAKEISYENTQISRAIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Homo sapiens UDP-glucose ceramide
/note="Homo sapiens UDP-glucose ceramide
glucosyltransferase-like 1, mRNA (cDNA clone MGC:46056
IMAGE:5492334), complete cds.; H_NH0462M09.1
This gene was based on gi(26958809)
Continued from H_NH0398G09.1"
The clone sequenced to the right is RP11-480N9. Actual start this clone is at base position 1 of RP11-462M9; actual end is base position 176075 of RP11-462M9.
                                                                                                                                           The sequence H NH0462M09 from base positions 164804 to 164876 165220 to 1652\overline{9}8 are represented by sequence derived from PCR BAC DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="CpG island (%GC=69.9, o/e=0.83, #CpGs=96)"
complement[113972. .165192)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (join(113972. .115384,164551. .165192))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(114676. .115384,164551.
/gene="HS6ST1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="unknown"
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                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="HS6ST1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="HS6ST1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
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                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted (09-AUG-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
(bases 1 to 176075)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (09-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (15-APR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (21-APR-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 511-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 0); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MO 63108, USA
On Apr 15, 2001 this sequence version replaced gi:13431206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                       and Belter, E.
BAC clone RP11-462M9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Genetics,
Park Avenue, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WUGSC
Web site: http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: H_NH0462M09
                                                                                                                                               Hominidae; Homo.

1 (bases 1 to 176075)

Hawkins, M., Maupin, R., Le, T. an
The sequence of Homo sapiens BA
Unpublished (2001)

2 (bases 1 to 176075)

Waterston, R.H.
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University, 4444 Forest
6 (bases 1 to 176075)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 176075)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 (bases 1 to 176075)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston, R.
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/note="Homo sapiens heparan sulfate 6-0-sulfotransferase 1

(HS6ST1), mRNA.; H NH0462M09.2 This gene was based on gi(4758565)"

/protein_id="AAY14736.1"

NEIGHBORING SEQUENCE INFORMATION:

/codon_start=1 /product="unknown"

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86100. .86270,90809. .93460)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JULN (44403. 44575,44793. .44961,61407. .61488,63301. .63380,
67645. .>67856)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="RP11-131A5.1-002"
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67645. .>67856)
/gene="RAD23B"
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9 RPII-131A5 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /locus tag="RP11-131A5.1-001"
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86100. .86270,90809. .93460)
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86100. .86270,90809. .90922)
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/note="match: proteins: AAH27747 CAD13275 P54727 P54728
Q8WUB0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /jocus tag="RP11-131A5.1-001"
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AW653949.1 BE018477.1 BE048265.1 BM663704.1 BM977864.1
BQ000373.1 BQ002122.1 BQ022617.1 BQ045177.1 BQ772030.1
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note="Sequence from overlapping clone bA417L14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12357. 42785
'note="Sequence from overlapping clone bA417L14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="Clone_left_end: RP11-131A5"
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                                                                                                                                                                                                            ------ Genome Center
Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                         Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="RPCI-11.1"
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                                                                                                                                                                                                                                                                       code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91675 GATGTTCAAAGTGAATATTGATATAGTTAATATTTTACCATATATTTTTTACTATT 91616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91676
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Clone requests: clonerequest@sanger.ac.uk
On Mar 24, 2001 this sequence version replaced gi:13276998.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                   /trānslation="MVERASKFVLVVAGSVCFMLILYQYAGPGLSLGAPGGRAPPDDL
DLFPTPDPHYEKKYYFPVRELERSLRFDMKGDDVIVFLHIQKTGGTTFGRHLVQNVRL
EVPCDCRPGQKKCTCYRPNRRETWLFSRFSTGWSCGLHADWTELTNCVPGVLDRRDSA
                                                                                                                      ALRTPRKFYYITLLRDPVSRYLSEWRHVQRGATWKTSLHMCDGRTPTPEELPFCYEGT
WAGGCTLGEFROCPYNLANNRQYRMLADLSLVGCYNLSFI PEGKRAQLLESAKKGULR
GMAFGCLTEFGRKTOTLERTFRULKFI RPFMOYNSTRAGGVEVDEDTIRR IEELMULD
MQLYDYAKDLFQQRYQYKRQLERREQRLRSREERLLHRAKEALPREDADEPGRVPTED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TCGAACTTCAAACCTCAGGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTAGGATTACAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTCTTACATCTTCAAGTGCTAGAAAT 180
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Human DNA sequence from clone RP11-131A5 on chromosome 9q32-34.11
Contains the RAD23B gene for RA23B homolog B (S. cerevisiae) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCGGCTAATTTTGTATCTTTTAGTAGAGGCGTTCCTCCATGTTGGTCAGGCTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GCTTATGAAAACGAAAAAAAGAATTATTAAGAGTAATTATAAAGAAACACTCATT--TTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Gaps
                                                                                                                                                                                                                                                              114711. .115359

/note="CpG island (%GC=65.8, o/e=0.72, #CpGs=60)"

/note="CpG island (%GC=71.7, o/e=0.80, #CpGs=269)"

/note="CpG island (%GC=71.7, o/e=0.96, #CpGs=85)"

/note="CpG_island (%GC=74.4, o/e=0.96, #CpGs=85)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 176075;
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HTG; CpG island; HR23B; RAD23B; UV excision repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 36.4%; Score 130.8; DB 8
Best Local Similarity 67.2%; Pred. No. 1.1e-18;
Matches 215; Conservative 0; Mismatches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 three CpG islands, complete sequence.
           xref="GI:62822187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91555 TGAGGTTTTAATTGAGATTG 91536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 AAAGGAGTATAATTAAATTG 318
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1 (bases 1 to 162509)
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KEYWORDS
SOURCE
ORGANISM
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1 (bases 1 to 568)

Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sujayama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 6845 09-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAITO,
JUNICHI YAWAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAWA,AI WAKAMATSU,
KEIICHI NAGAI,TETSUJI OTSUKI
LFEDATSALVTGQSYENMVTEIMSMGYEREQVIAALRASFNNPDRAVEYLLMIIVKTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGAACTTCAAACCTCAGGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTAGGATTACAG 120
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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28-JUL-2000 JP 2000280990
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
                                                                                                                                                                                                                                                                                                                                                                   /locus tag="RP11-131A5.1-004"
/note="Single clone region. Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCCGGCTAATTTTGTATCTTTTAGTAGACGCGTTCCTCCATGTTGGTCAGGCTGGTC
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Primer for synthesizing full-length cDNA and use thereof.
BDIS2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                /locus tag="RP11-131A5.1-004"
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                                                                                                                         /locus tag="RP11-131A5.1-004"
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84699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.5%; Score 127.4; DB 8 llarity 89.7%; Pred. No. 6.2e-18; Conservative 0; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /locus_tag="RP11-131A5.1-004"
92159
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92287._.92292
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JP 2002191363-A/6845
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JP 2002191363-A/6845.
Homo sapiens (human)
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/gene="RAD23B"
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                                            NKKKKQPLLGK"
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Matches 148; Conserv
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Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: vega@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk on Nov 15, 2001 this sequence version replaced gi:16444731.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13

RPI1-469L23 is from the library PRCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                          Human DNA sequence from clone RP11-469L23 on chromosome 13 Contains the ALOXXAP gene for arachidonate 5-lipoxygenase-activating protein (FLAP) and a novel gene, complete sequence.
AL512642.18 GI:16944077
HTG; ALOXSAP; FLAP.
How sapiens (human)
Home sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
GCGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTTCTTACATCTTCAAGTGCTAGAAAT 180
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Clone_right_end: RP11-121019"
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65191. .65666)
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/locus_tag="RP11-469L23.1-001"
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Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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join(36755. .36922,453
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1 (bases 1 to 139255)
Mashreghi-Mohammadi, M.
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                                                                                                                                      GTTCAGAGAAA 332
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VECTOR: pBACe3.6
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  PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                  C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00
Primer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
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                                                                                                                                                     /organism='Homo sapiens (human)'.
Location/Qualifiers
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larity 79.1%; Pred. No. 9.2e-18;
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Sequence 6845 from Patent EP1074617.
AX871940
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                                                                                                                                                                                                              1. .568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 79.1
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 GTTCAGAGAAA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTTATGAAAA 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                           source
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151; Conserv
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Best Local S:
Matches 151
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ORGANISM
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VERSION
KEYWORDS
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                                                                                                                                                                                          FEATURES
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HTG 30-SEP-2001
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                          Homo sapiens chromosome 1 clone RP11-296F18, 19 unordered pieces. AL451053 AC027437
AL451053.3 GI:13872392
HTG; HTGS PHASE1; HTGS_CANCELLED.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 62% of reads
Consensus quality: 142362 bases at least Q40
Consensus quality: 144065 bases at least Q40
Consensus quality: 145103 bases at least Q30
Consensus quality: 145103 bases at least Q20
Insert size: 164885; sum-of-contigs
Insert size: 163808; 8.2% error; agarose-fp
Quality coverage: 6.17x in Q20 bases; sum-of-contigs Quality
coverage: 5.94x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (19-28P-2001) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (19-28P-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On or before May 15, 2001 this sequence version replaced
gi:7637297, gi:13785412.
Draft Sequence Produced by Whitehead Institute/MIT Center for
Genome Research, 320 Charles Street,
Cambridge, MA 02141, USA
123699 CGTGAGCCACCACCCAGCCAAGCAATTCCATTTTCAAAAGCTTTTAAT 123650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   f 100 bp
g of 17920 bp in length
f 100 bp
g of 9598 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 3047 bp in length
gap of 100 bp
contig of 8653 bp in length
gap of 100 bp
contig of 6717 bp in length
gap of 100 bp
contig of 1720 bp in length
gap of 100 bp
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gap of 100 bp
contig of 2467 bp in length
gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: humquery@sanger.ac.uk
------- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: bA296P18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
gap of
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18528
18628
36548
46246
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49691
49791
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64762
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72598
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                                                                                                                                                                                                                                                                                                                                                          Hall, R.
                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                     RESULT 13
                                                                                        AL451053
LOCUS
                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                VERSION
    셤
                                                                                                                                                                                                                   join(36853. .36922,45307. .45406,53299. .53369,57191. .57272,65191. .65353)
/gene="ALOX5AP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .36922,45307. .45406,53299. .53369,57191. .57272,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MOQETYCNVVILAIVTLISVVQNGFFAHKVEHESRTQNGRSFQR
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GERTQSTPGYIFGKRIILFFLFLMSVAGIFNYYLIFFFGSDFENYIKTISTTISPLLLI
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B18471373 BF796002 BG435742 BG537585 BG548714 BG569867
B1911044 BM972232 BQ016599 BQ287903
match: cDNAs: BC018538 BC026209 M96552 M96553 M96554
M96556 M96557 X52195"
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/protein_id="CAH74084.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Single clone region. Sequence from uni-directional degre big dye terminator reads only."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 CGAACTTCAAACCTCAGGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTAGGATTACAGG
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/noce="match: proteins: AAH18538 P20291 P20292 P30353
930354 P30355 P30356 P30357 P30358 Q9D138"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /locus tag="RP11-469L23.1-001"
/note="Single clone region. Assembly confirmed by restriction digest data."
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/gene="ALOX5AP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Single clone region. Assembly confirmed by restriction digest data."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.3%; Score 126.8; DB 8; Length 139255;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(104453. .104839,111374. .111892)

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join(104453. .104839,111374. .111892)

/locus tag="RP11-465123.2-001"

/note="match: EST8: BI818416 BI818490"
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/note="Clone_right_end: RP11-469L23"
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join(43583. .43792,45307. .45643)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="RP11-469L23.1-001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     xref="InterPro:IPR001446"
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Best Local Similarity 84.1<sup>1</sup>
Matches 143; Conservative
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             mRNA
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contig of 7877 bp in length gap of 100 bp contig of 21514 bp in length gap of 100 bp contig of 6640 bp in length contig of 8986 bp in length contig of 8986 bp in length gap of 100 bp
                                                                                                                                                                                                        95 132520: Contig of 3826 bp in length
21 132620: gap of 100 bp
21 141424: Contig of 8804 bp in length
35 141524: gap of 100 bp
35 148285: Contig of 6761 bp in length.
36 14000 Location/Qualifiers
                                                                                                                                                                 contrig of 1999 bp in length gap of 100 bp contig of 3826 bp in length contig of 3826 bp in length
bp in length
                100 bp
of 7877 bp in length
                                                                                                                                                       2183 bp in length
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84873. 106386
/note="assembly_fragment:00242"
11326487. 113126
/note="assembly_fragment:00635"
113227. 122212
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36648. .46245.
/notes assembly fragment:02197 fragment chain:2"
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1. .3047
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fragment chain:1"
3148. .1710
/note="assembly_fragment:00530
fragment_chain:1"
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70131. 72597

fragment chain:4"

72698. 76795

700ce=assembly fragment:01354

fragment chain:4"
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Direct Submission

Submitted (17-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk

On Apr 19, 2002 this sequence version replaced gi:20196555.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, SMISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Purther information can be found at http://www.sanger.ac.uk/HGPChr1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National DNA sequence from clone RPII-316M1 on chromosome 1 Contains the SETDB1 gene for SET domain, bifurcated 1, the LASS2 gene for LAG1 longevity segurance homolog (s. cerevisiae), the ANXA9 gene for annexin A9, the gene for a novel protein (FLJ11280), the gene for TcD37 homolog (HTCD37), the BNIPL gene for BCL2/adenovirus E1B 19kD interacting protein 11ke, the gene for a novel protein (FLJ20519), the gene for small protein effector 1 of Cdc42 (SPECI), the gene for ALL1-fused gene from chromosome 1q (AFLQ), two novel genes, the 5' end of a novel gene (MGC29891) and two CpG islands, complete sequence.

N ALS90133 ACC73204
ALS90133 ACC73204
HTG; AR1Q; ANXA9; BNIPL; CDC42; CpG island; FLJ11280; FLJ20519; HTCD37; LASS2; MGC29891; SETDB1; SPEC1; TCD37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GCGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTCTTACATCTTCAAGTGCTAGAAAT 180
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                  TCGAACTTCAAACCTCAGGTGATCCGCCCCCCCCCCCAAAGTGCTAGGATTACAG
                                                                                                                                                                       Gaps
                                                                                                          Score 126.8; DB 14; Length 148285; Pred. No. 8.4e-18; O; Mismatches 47; Indels 0; G
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141525. .148285
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AUTHORS
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FEATURES

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              as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. RPII-316M1 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                 Draft Sequence Produced by Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA.

http://genome.wustl.edu/gsc/index.shtml.
Location/Qualifiers
1. 192096
/organism=Homo sapiens"
/mol type="Remomic DNA"
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|oin(12484. _12541,13897. .14167,16160. .16230)
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36226 TCGAACTCCCGACCTCAGGTGATCCACCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAG 36167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36166 GCATGAGCCACCGCCCGGCCTAACÁTCTCTATTTCAACAGTATACCTTTTCCTAAAAT 36107
                                   LDHIESVENFKEĞYESDAPCSSDSSGVDLKDQEDGNSGTEDPEESNDDSSDDNFCKDE
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ESCYIIDAKLEGNLGRYLNHSCSPNLFVQNVFVDTHDLRFPWVAFFASKRIRAGTELT
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                                                                                                                                                                          IKDEGDIKQAKKEDTDDRNKMSVVTESSRNYGYNPSPVKPEGLRRPPSKTSMHQSRRL
HGLQVRLQLFKTQNKGWGIRCLDDIAKGSFVCIYAGKILTDDFADKEGLEMGDEYFAN
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match 35.3%; Score 126.8; DB 8; Length : Best Local Similarity 76.7%; Pred. No. 8.3e-18; Matches 155; Conservative 0; Mismatches 47; Indels
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유 ð 셤 ò 셤 ò

linear PRI 15-MAR-2003 Homo sapiens 12 BAC RP11-112B10 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
AC117378 AC021586
AC117378.8 GI:23346656 Homo sapiens (human) VERSION KEYWORDS SOURCE ORGANISM AC117378/c DEFINITION ACCESSION REFERENCE AUTHORS

셤

Homo saplens Butheria; Craniata; Vertebrata; Etteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Etteleostomi; Hominidae; Homo.

1 (Dases 1 to 110459)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Areb., T.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bubay, C., Burch, P., Burkett, C., Areb., T., Baryant, N.P., Bubay, C., Burch, P., Burkett, C., Burchl, K., Bowie, S., Burkett, C., Burchl, K., Bowie, S., Burkett, C., Burchl, K., Bowie, S., Charch, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Chen, G., Cow, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D. A., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D. A., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D. A., David, R., Barchart, C., Edgar, D., Edwards, C.C., Elbaj, C., Emerling, S., Barchart, C., Edgar, D., Edwards, C.C., Elbaj, C., Emerling, S., Barchart, C., Edgar, D., Edwards, C., C., Elbaj, C., Emerling, S., Haniton, K., Han, J., Harris, K., Hart, M., Havlak, P., Hanle, S., Merrandez, J., Hernandez, O., Hodgson, A., Hearis, K., Hart, M., Havlak, P., Hume, J., Loshikhes, I., Jacobson, B., Jia, Y., Johnson, R., Joliver, S., Joudah, S., Karlsson, E., Kells, Y., Lucier, R., Joulseged, H., Lozado, R., Lucier, R., Lous, B., Martinale, R., Martinaz, E., Massey, E., Marchell, T., Martin, R., Martinale, R., Martinaz, E., Massey, E., Marchell, T., Martin, R., Martinale, A., Miner, Z., Mitchell, T., Mortson, D., Newtson, J., Nguyen, N., Nguyen, N.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley, K.C.

Direct Submission

Submitted (19-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

4 (bases 1 to 110459)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-MRR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 30, 2002 This sequence version replaced gi:21490136. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10.APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (30-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 110459)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (Dases 1 to 110459)
Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for clones and 3 reads with no ambiguities. If the sequence quality for

rpt family="AluYb8"

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repeat_region
                                                            repeat_region
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                                                          QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

http://www.hgsc.bcm.tmc.edu.8088/quality.info/genbank.annotation.ht
a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                               1. .2002

// note= overlaps bases 91579. .93582 of clone AC090681"

// function="clone overlap"

complement (538. .637)

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complement (4484. .4756)

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complement (5469. .5762)

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complement (5763. .6055)

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29634 TCGAACTCCCAACCTCAGGTGATTCGCCCGCCTCGGCCTCCCAAATGCTGGGATTACAG 29575
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Best Local Similarity 84.9%; Pred. No. 1.3e-17;
Matches 141; Conservative 0; Mismatches 25; Indels 0;
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5.1.7
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359
GenCore version
Copyright (c) 1993 - 2006
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summaries

N_Geneseq_21:* 1: geneseqn198

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		Description	Aal41898 Human GA7	Aah10010 Human cDN	Continuation (4 of	Continuation (4 of	Abz70301 Human tyr	Aak68705 Human imm	Abv13839 Human pro	Adl08116 Human gen	Aak78202 Human imm	Adz70075 Human ins	Ads36450 Human aut	Abd32707 Human can	Abl83966 Human ova	Acf91521 Human SIR	Aas90976 DNA encod	Abv25066 Human pro	Aea61123 Human PDE	Aak67239 Human imm	Adz57848 Human Alu
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		DB	4	4	12	13	v	4	Ŋ	12	4	14	13	13	ø	13	S	2	14	4	11
		Query Aatch Length DB	4282	568	98800	98800	1744	344	438	160361	22651	313001	321019	329019	381	546	556	3470	122673	30393	291
	æ	Query	100.0	35.4	35.3	35.3	34.7	34.5	34.5	34.1	34.0	34.0	34.0	34.0	33.9	33.9	33.9	33.9	33.9	33.8	33.8
		Score	359	127	126.8	126.8	124.4	123.8	123.8	122.4	122.2	122	122	122	121.8	121.8	121.8	121.8	121.8	121.4	121.2
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Abz73859 Secreted	Ada98513 Human sec	Ada44266 Human sec	Adc20639 Human sec	Adf10839 Human sec	Abz67436 Human sec	Aak90274 Human dig	Aai57654 Human col	Abs99831 Genomic D	Adb92984 Human col	Adol5908 4 synthes	Aak73470 Human imm	Aak73471 Human imm	Aea61178 Human GPR	Adl13758 Osteoarth	Aah14445 Human cDN	Abx04191 Human mRN	Aak87132 Human imm	Abd32581 Human can	Adh59595 Alu-repea	Aak79905 Human imm	Aak79904 Human imm	Aea61110 Human CDA	Human	Ads94372 Human 5-1	Abk83460 Human cDN	
ABZ73859	ADA98513	ADA44266	ADC20639	ADF10839) ABZ67436	AAK90274	AA157654	ABS99831) ADB92984	AD015908	AAK73470	AAK73471	H AEA61178) ADL13758	AAH14445	ABX04191	AAK87132	3 ABD32581	ADH59595	AAK79905	AAK79904	1 AEA61110	2 ADN06353 0	3 ADS94372 ⁰	ABK83460 _	
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3.8	3.8	33.8	33.8	33.8	33.8	33.6	33.6	3.6	33.6	33.6	33.6	3.6	3.6	33.5	33.5	33.5	3.5	33.5	33.4	33.4	33.4	33.4	33.4	33.4	3.4	
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121.2	121.2	121.2	121.2	121.2	121.2	120.8	120.8	120.8	120.8	120.8	120.8	120.8	120.8	120.4	120.2	120.2	120.2	120.2	120	120	120	120	120	120	120	
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ALIGNMENTS

Human; GA733-2 gene promoter; gene; epithelial glycoprotein-2; EGP-2; pan-carcinoma associated antigen; cancer; carcinoma selective expression; treatment evaluation; non-squamous epithelium disease; carcinogenesis; transgenic animal; ds; gene therapy. Human GA733-2 gene (encoding human epithelial glycoprotein-2) promoter. Harmsen MC; Ruiters MHJ, Dokter WHA; AAL41898 standard; DNA; 4282 BP De Leij LFMH, Mclaughlin PMJ, Van Der Molen H, Terpstra P, 01-MAR-2000; 2000EP-00200728. 01-MAR-2000; 2000EP-00200728. (UYGR-) RIJKSUNIV GRONINGEN (first entry) WPI; 2001-591523/67. EP1130106-A1. Homo sapiens 03-MAY-2002 05-SEP-2001. AAL41898; RESULT 1

Novel isolated and/or recombinant nucleic acid having tissue specific promoter derived from epithelial glycoprotein 2 gene, that allows expression of desired nucleic acid in cancer cell, specifically carcinoma

Claim 3; Fig 1; 21pp; English.

The invention comprises the promoter sequence of the human GA733-2 gene. The GA733-2 gene encodes human epithelial glycoprotein-2 (EGP-2), which is a pan-carcinoma associated antigen. The GA733-2 gene promoter allows

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                                                                                                                                                                                                                                                            1188 CCCGGCTAATTTTGTATCTTTTAGTAGAGGGCGTTCCTCCCATGTTGGTCAGGCTGGTC 3247
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the expression of a nucleic acid of interest in a cancer cell, where the expression within the cancer cell is carcinoma selective. The GA733-2 gene promoter sequence is useful in the treatment of cancer and in evaluating the treatment of a disease (e.g. a disease of the non-squamous epithelium, such as carcinogenesis). The GA733-2 gene promoter can also be used in the production of host cells and a transgenic animal. The present nucleotide sequence represents the GA733-2 gene promoter sequence
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                                                                                                                                             Sequence 4282 BP; 1115 A; 1031 C; 976 G; 1160 T; 0 U; 0 Other;
                                                                                                                                                                           Length 4282;
                                                                                                                                                                                                          Indels
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Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 CCAAGAGGCCAAGATTTCTTCTTTCCTCTTCTTTTTTT
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                                                                                                                                                                           Score 359; DB 4;
Pred. No. 5.2e-70;
0; Mismatches 0;
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27-ANG-1999; 99JP-00300253.
11-JAN-22009; 2000JP-00118776.
09-MAY-2000; 2000JP-00241899.
                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 359; Conservative 0
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                                                                                                                 the invention
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from base 300001 (Human FLAP genomic DNA SEQ ID NO:1. 
 LOCUS ADN06353 Accession Adn06353
                                                                                                                                    The present invention describes primer sets for synthesising 5602 full-

[a] an oligo-dr primer and an oligonucleotide complementary to the

[c] an oligo-dr primer and an oligonucleotide complementary to the

[c] complementary strand of a polynucleotide which comprises one of the 5602

[c] complementary strand of a polynucleotide which comprises one of the 5602

[c] concloside comprises at least 15 nucleotides; or (b) a combination

[c] c] oligonucleotide comprises as sequence complementary to the

[c] complementary strand of a polynucleotide which comprises a 5'-end

[c] sequence and an oligonucleotide comprising a sequence complementary to a

[c] complementary strand of a polynucleotide which comprises a 5'-end

[c] sequence and an oligonucleotide comprising a sequence, where the

[c] complementary strand of a polynucleotide which comprises a 5'-end

[c] sequence and an oligonucleotide comprises and the complementary to a

[c] complementary strand of a polynucleotide sudden those defined in the

[c] c] complementary sets as least 15 nucleotides and the combination of

[c] the 5'-end sequence[3'-end sequence is selected from those defined in the

[c] specification. The primer sets can be used in antisense therapy and in

[c] specification and/or diagnosis of the abnormality of the proteins encoded by

[c] che full-length cDNAs. The primers are also useful for the

[c] cDNAs easily without any specialised methods. AAH03146 to AAH13628

[c] chessent human amino acid sequences; and AAH13632 represent

[c] coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 CGAACTICAAACCICAGGTGTCCGCCCGCCTCGGCCTCCCAAAGTGCTAGGATTACAGG
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                                                                                                        English.
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Pred. No. 1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 568 BP; 154 A; 138 C; 128 G; 141 T; 0 U; 7 Other;
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                                                                                                        Listing;
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Pred. No. 2.9e-18;
0; Mismatches 27;
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0; Mismatches
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210000
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fragments
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79.1%;
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84.1%;
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WP Fragment Name
B ADN06353_0
WP ADN06353_1
WP ADN06553_3
WP ADN06553_3
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                                                                                                        Claim 3;
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1444 TCGAACTCCTGACCTCATGTGATCCGCCCTCGGCTTCCCAAAGTGCTGGGATTACAG 1503
                                                                                                                                                         1384 CCCGGCTAATTTTTGTATTTTTAGTAGAGGGGGTTTCTCCCATGTTGGTCAGGCTGGTC 1443
                                                                                                                                                                                           61 TCGAACTTCAAACCTCAGGTGATCCGCCCCCCTCGGCCTCCCAAAGTGCTAGGATTACAG 120
The present sequence is the coding sequence for human tyrosinase 10.01. The protein can be used for treating diseases such as cancer and HIV
                                                                                                                                      CCCGGCTAATTTTTGTATTTTAGTAGAGGGCGTTCCTCCATGTTGGTCAGGCTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23517.
                                                                                                             Gaps
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                                                                               Score 124.4; DB 6; Length 1744; Pred. No. 4.7e-18;
                                                    Sequence 1744 BP; 354 A; 478 C; 476 G; 436 T; 0 U; 0 Other;
                                                                                                             21; Indels
                                                                                                                                                                                                                                                                  GCGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTCT 158
                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-APR-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0198123P.
28-JUN-2000; 2000US-0214886P.
30-JUN-2000; 2000US-0214886P.
30-JUN-2000; 2000US-0214886P.
11-JUL-2000; 2000US-0216847P.
11-JUL-2000; 2000US-0216847P.
11-JUL-2000; 2000US-021889P.
14-JUL-2000; 2000US-021899P.
26-JUL-2000; 2000US-0218290P.
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04-FEB-2000; 2000US-0186528P.
24-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0186550P.
16-MAR-2000; 2000US-018974P.
17-MAR-2000; 2000US-0199076P.
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2000US-0220963P.
2000US-0220964P.
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2000US-0225757P.
2000US-0225758P.
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14-AUG-2000; 2000US-0225214P.
14-AUG-2000; 2000US-0225214P.
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                                                                                Query Match 34.7%;
Best Local Similarity 86.7%;
Matches 137; Conservative
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ADS94372 3/C

ADS94372 from base 300001 (Human 5-lipoxygenase activating prot Continuation (4 of 4) of ADS94372 from base 300001 (Human 5-lipoxygenase activating prot WP Sequence split into 4 fragments LOCUS ADS94372 Accession Ads94372

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                               122 CGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTCTTACATCTTCAAGT 171
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Pred. No. 2.9
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                                                                                                                                                                                                                                          Query Match 35.3%;
Best Local Similarity 84.1%;
Matches 143; Conservative
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ADS94372_2
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2000US-0241786P.
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08-NOV-2000;
08-NOV-2000;
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06-SEP-2000;
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08-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
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AAK54951 to AAK64702 encode the human immune/haemacopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) cypynucleotides may be used to produce the secreted (I), by inserting the polynucleotides may be used to produce the secreted (I), by inserting the collynucleotides may be used to produce the secreted (I), by inserting the protein. (I) proteins and polynucleotides may be used to prevent, cancers and cancer metastesses of haematopoietic-related diseases, especially cancer metastesses of haematopoietic-artived cells. AAK64703 cancers and cancer metastesses of haematopoietic antigen genomic comparation the present invention. AAK54912 to AAK87691 and AAM82169 cerpresent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 CCCAGCTAATTTTTGTATTTTTTAGTAGAGATGGGGTTTCTCCATGTTGGTCGGCTGGTC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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34.5%; Score 123.8; DB 4; Length 344;
Best Local Similarity 83.8%; Pred. No. 4.8e-18;
Matches 140; Conservative 0; Mismatches 27; Indels 0;
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                                                          2000US-0249209P.
2000US-0249210P.
2000US-0249211P.
2000US-0249212P.
2000US-0249213P.
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2000US-0249297P.
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2000US-0249216P.
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2000US-0249245P.
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2000US-0251479P.
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2000US-0251869P.
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01-DEC-2000; 2
05-DEC-2000; 2
05-DEC-2000; 2
05-DEC-2000; 2
                                                             17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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CGAACTTCAAACCTCAGGTGATCCGCCCCCCTCGGCCTCCCAAAGTGCTAGGATTACAGG

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic optential of a compound; (f) assessing the prostate call carcinogenic potential of a compound; g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient
                    Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                      GCGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTCTTACATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate expression marker cDNA 13830.
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2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
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25-MAY-2000;
09-JUN-2000;
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13-DEC-2000;
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The invention relates to determining whether a subject has, or is at risk of developing, an abnormally low high density lipoprotein-C (HDL-C) level comprises determining whether the subject has an allelic variant of a polymorphic region from any of 27 genes (alleles listed in Table 5 of the specification). Also included are determining whether a male subject has, or is at risk of developing, an abnormally low HDL-C level, comprising determining whether the male subject has an allelic variant of a polymorphic region listed in Table 5 which is associated with abnormally low HDL-C levels in males, and determining whether a female subject has, or is at risk of developing, an abnormally low HDL-C level, comprising determining whether the female subject has an allelic variant of a determining whether the females. The allelic variant of a low HDL-C levels in females. The allelic variant in determining whether a clow HDL-C levels in females. The allelic variant in determining whether a subject has, or is at risk of developing, an abnormally low HDL-C level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining whether a subject has, or is at risk of developing, an abnormally low high density lipoprotein-C (HDL-C) level comprises detecting an allelic variant of a polymorphic region from any of a set of
                                                                                                         241
           228
                                            181
                                                                Human; ds; SND; single nucleotide polymorphism;
high denaity lipoprotein-C; HDL-C; vascular disease; metabolic disease;
coronary artery disease; gene.
182 CTTATGAAAACGAAAAAAAGAATTATTAAGAGTAATTATAAAGAAACACTCATTTTCTTCC
                                            CGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTCTTACATCTTCAAGTGCTAGAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/standard_name= "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                          Human gene associated with low HDL-C FABP-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 35; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                              ADL08116 standard; DNA; 160361 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-SEP-2002; 2002US-00235192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-SEP-2002; 2002US-00235192.
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (VITI-) VITIVITY INC
                                                                                                                                                                             242 CAAGAGA 248
                                                                                                                                                                                                              349 AAATACA 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                variation
                                                                                                                                                                                                                                                                                                                              ADL08116;
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                 169
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ADL08116
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CCGGCTAATTTTGTATCTTTTAGTAGACGCCGTTCCTCCATGTTGGTCAGGCTGGTCT

Conservative

Best Local Similarity Matches 170; Conserv

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157896 CCCGGCTAATTTTGTATTTTTAGTAGAGGTGGGGTTTTCTCCATGTTGGTCAGGCTGGTC 157955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157956 TCAAACTCCCGACCTCAGGTGATCCGCCCCCCCTCCCCCAAAGTGTTGGGATTACAG 158015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158016 GCGCGAGCCACCGCGCCCGGCTGAGACCACTTCTGTCTTTAAAGGCTCCTGCTAAT 158075
is APOA 1 CC, CD14 1 CT, COL5A2 1 GG, EDNRB 1 AG or AA, FABP3 1 CT, GBE1 allalic variant in determining whether a male subject has, or is at risk of developing, an abnormally low HDL-C level, LRP1 3 CC or CT, PAIZ 4 GG, or PPARG 1 CG, or their complements. The allelic variants are also COL5A2 or PPARG 1 CG, or their complements. The allelic variants are also COL5A2 or GC, CD14 1 CT or CC, and FABP3 1 CT, in combination, or their complements. The methods are useful for diagnosing (a predisposition to) abnormally low levels of low high density lipoprotein-C (HDL-C) in a subject, The methods are useful in diagnosing (a predisposition to) or prognosticating diseases and disorders associated with abnormal lipid levels such as vascular and metabolic diseases, e.g., coronary artery diseases. The present sequence is a human gene containing a SNP (single mucleotide polymorphism associated with low high density lipoprotein-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TCGAACTTCAAACCTCAGGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTAGGATTACAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTCTTACATCTTCAAGTGCTAGAAAT 180
                                                                                                                                                                                                                                                                                                       Sequence 160361 BP; 43435 A; 35277 C; 35459 G; 45990 T; 0 U; 200 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                            CCCGCCTAATTTTGTATCTTTTAGTAGAGGCGGTTCCTCCATGTTGGTCAGGCTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, immune, haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33014.
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Pred. No. 3e-17;
0; Mismatches 36; Indels 0; G
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AC AAK78202;
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DT
O7-NOV-2001 (first entry)
XX

Human immune/haematopoietic antigen
XX

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Human; immune, haematopoietic; immu
XX

Human; immune, haematopoietic; immu
XX

W
Human; immune, haematopoietic; immu
XX

XX

Homo sapiens.
XX

D9-AUG-2001.
XX

PF
17-JAN-2001; 2001WO-US001354.
XX

PF
17-JAN-2000; 2000US-0180628P.
PR
24-FEB-2000; 2000US-0180628P.
PR
24-FEB-2000; 2000US-0180628P.
PR
17-MAR-2000; 2000US-018064P.
PR
17-MAR-2000; 2000US-0189874P.
PR
17-MAR-2000; 2000US-0189874P.
PR
17-MAR-2000; 2000US-0189874P.
PR
18-APR-2000; 2000US-0189874P.
PR
19-MAY-2000; 2000US-0189874P.
PR
19-MAY-2000; 2000US-0189878P.
PR
19-MAY-2000; 2000US-015135P.
PR
10-JUL-2000; 2000US-021487P.
PR
11-JUL-2000; 2000US-021487P.
PR
11-JUL-2000; 2000US-0217487P.
PR
11-JUL-2000; 2000US-0217487P.
PR
26-JUL-2000; 2000US-0220963P.
PR
26-JUL-2000; 2000US-0220964P.
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Best Local Similarity 80.0
Matches 144; Conservative
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PR 14-AUG-2000; 2000US-0224519FP PR 14-AUG-2000; 2000US-0225513P. PR 14-AUG-2000; 2000US-0225513P. PR 14-AUG-2000; 2000US-0225513P. PR 14-AUG-2000; 2000US-022556FP. PR 14-AUG-2000; 2000US-022556FP. PR 14-AUG-2000; 2000US-022556FP. PR 14-AUG-2000; 2000US-022557FP. PR 22-AUG-2000; 2000US-022557FP. PR 22-AUG-2000; 2000US-02257FP. PR 23-AUG-2000; 2000US-02237FP. PR 23-AUG-2000; 2000US-0231744P. PR 23-AUG-2000; 2000US-0231749P. PR 23-AUG-2000; 2000US-0231749P. PR 23-AUG-2000S-0231749P. PR 23-AUG-2000S-0231749P. PR 23-AUG-2000S-0231749P. PR 2
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) copynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a post cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the screted diseases, especially diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54922 to AAK54550 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 33014; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben SM
                                                                                                                  2000US-0246609P.
2000US-0246610P.
2000US-0246611P.
2000US-0246613P.
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2000US-0249213P
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                                                  08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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01-DEC-2000;
01-DEC-2000;
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17-NOV-2000;
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                                                                                                                          61 TCGAACTTCAAACCTCAGGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTAGGATTACAG 120
                                                                         9
represent sequences used in the exemplification of the present invention
                                                                                           4383 CCCGCCTAATTTTGTATTTTTTAGTAGATGGGGTTTCTCCATGTTGGTCAGGCTGGTC
                                                                         1 CCCGGCTAATTTTGTATCTTTTAGTAGACGCGCTTCCTCCATGTTGGTCAGGCTGGTC
                                                                                                                                                                                                                                                                          Human insulin-like growth factor 1 receptor (IGF-IR) gene - SEQ ID 1.
                  Sequence 22651 BP; 5939 A; 5107 C; 5360 G; 6245 T; 0 U; 0 Other;
                                   Score 122.2; DB 4; Length 22651;
Pred. No. 2.3e-17;
0; Mismatches 13; Indels 0;
                                                                                                                                                                                                                                                                                           cardiant;
                                                                                                                                                                                                                                                                                                                                                                                *tag= c
product= "Human IGF-IR protein"
                                                                                                                                                                                                                                                                                            SNP detection, diagnosis, cardiac hypertrophy, or insulin-like growth factor 1 receptor; gene; ds.
                                                                                                                                                                  4263 GCGTGAGCCACCGCACCCAGCCT 4241
                                                                                                                                                   121 GCGTGAGCCACGCGCTCAGCCT 143
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                RESULT 10
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ID ADZ70075 standard; DNA; 313001 BP.
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/number= 3
250716. .250864
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/number= 2
62067. .245283
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/*tag= d
/number= 1
61521. .62066
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.311401
                                     Query Match
Best Local Similarity 90.9%;
Matches 130; Conservative
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/number=
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exon

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/*teg42. .270090
269923. .270090
269923. .270090
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165058 cdaacrecreacereadrearedeceeceeceecreacereaagrecreagerracade 164999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises a method of testing hypertensive hypertrophy factor. The method involves determining the genotype of a polymorphism in the insulin-like growth factor 1 receptor (IGF-IR) gene of a subject, and determined the hypertensive cardiac hypertrophy factor based on the determined genotype. The method of the invention is useful for testing hypertensive cardiac hypertrophy factor, and thereby determining the risk of developing cardiac hypertrophy. The present DNA sequence represents the human IGF-IR gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGTGAGCCACCGCCTCAGCCTCGGAACACCTTTTTTTTACATCTTCAAGTGCTAGAAATG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Testing hypertensive cardiac hypertrophy factor, by determining genotype of polymorphism in insulin-like growth factor 1 receptor (IGF-IR) gene of subject and estimating based on determined genotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGGCTAATTTTGTATCTTTAGTAGAGACGCGTTCCTCCATGTTGGTCAGGCTGGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 313001 BP; 79741 A; 67002 C; 72630 G; 93626 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.0%; Score 122; DB 14; Length 313001; 76.8%; Pred. No. 4.2e-17; ive 0; Mismatches 45; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     (KOKU-) KOKURITSU JUNKANKI BYO CENT SOCHO.
(DOKU-) DOKURITSU GYOSEI HOJIN IYAKUHIN IRYO KIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 1; 19pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                  09-OCT-2003; 2003JP-00350960.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 76.8
Matches 149; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2005-326229/34.
P-PSDB; ADZ70089.
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The invention relates to an isolated nucleic acid comprising at least 10 contiguous nucleotides of any of the 233 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancerassociated proteins. Also included are an expression vector comprising the isolated nucleic acid cited above, a host cell comprising the isolated nucleic acid or expression vector, a microarray for detecting a cancerassociated (CA) nucleic acid comprising at least 10 contiguous nucleotides of any of the above comprising at least 10 contiguous nucleotides of any of the above comprising frame of a CA sequence selected from any of the 95 conpuncleotide sequences, an isolated polypeptide (encoded within complement), an isolated antibody, (or its antigen binding fragment) that complement), an isolated antibody, (or its antigen binding fragment) that complement), an isolated antibody, (or its antigen binding fragment) that complement) an isolated antibody or its antigen binding fragment continual antibody, a pharmaceutical composition comprising the above monoclonal antibody, a pharmaceutical composition comprising the above colls (comprising the antibody cited above, methods for dispnosing cancer or for detecting the presence or above, or cancer cells in an individual, a method for inhibiting growth of cancer cells in an individual, an enthod for delivering and the above individual, an enthod for delivering drawn continual and individual and in
in an individual, an electronic library comprising the above polynucleotide or polypeptide (or their fragments), methods of screening for anticancer activity or for a bioactive agent capable of modulating the activity of a CA protein (CAP), methods for detecting cancer associated with expression of a polypeptide in a test cell sample, a method for treating cancers and a method for inhibiting the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ds; cancer-associated protein; gene; cytostatic; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cancer-associated genomic DNA HD14-043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malandro MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          claim 16; seqid 277; 310pp; English.
                                                                                                                                                                                                                                                                                                      ABD32707 standard; DNA; 329019 BP
                                                                                                                                                          167455 AATATGAAAGCAAA 167442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 MAR-2003; 2003US-00388838.
15-APR-2003; 2003US-00417375.
13-UN-2003; 2003US-00461862.
15-SEP-2003; 2003US-00663431.
15-DEC-2003; 2003US-00737318.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2003US-00367094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SAGR-) SAGRES DISCOVERY INC
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leukaemia; lymphoma; CAP.
                                                                                                CTTATGAAAACGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-652914/63.
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                                                                                                                                                                                                                                                                                                                                                                                                                            18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morris DW,
                                                                                                   182
                                                                                                                                                                                                                                                                                                                                                                    ABD32707;
                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                   ABD32707,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises amino acid and coding sequences containing genetic polymorphisms associated with an altered risk of developing an autoimmune disease (e.g. rheumatoid arthritis). The invention further comprises a method of identifying an individual that has an altered risk of developing an autoimmune disease, comprising detecting a single and protein sequences of the invention are useful for disgnosting and treating autoimmune disease, such as rheumatoid arthritis, type 1 diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory bowel disease, psoriasis, thyroiditis, celiac disease, pernicious anaemia, asthma, vitiligo, glomerulonephritis, Grave's disease, pernicious mycarditis, Sjogren's disease, or primary systemic vascultis. The present nucleic acid represents a human autoimmune disease-related genomic DNA sequence of the invention NOTE: The present sequence is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 CGAACTTCAAACCTCAGGTGATCCGCCCTCGGCCTCCCAAAGTGCTAGGATTACAGG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 CGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTCTTACATCTTCAAGTGCTAGAAATG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    shown in the specification, but has been retrieved from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CCGGCTAATTTTGTATCTTTTAGTAGACGCGTTCCTCCATGTTGGTCAGGCTGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                     single nucleotide polymorphism detection; SNP detection; rheumatoid arthritis; type 1 diabetes; multiple sclerosis; systemic lupus erythematosus; inflammatory bowel disease; psoriasis; thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo; glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease; primary systemic vasculitis; ds.
                                                                                                                                                                                                                                                                                   Human autoimmune disease-related genomic DNA sequence - SEQ ID 1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid molecule comprises at least 8 contiguous nucleotides where one of the nucleotides is a single nucleotide polymorphism (SNP), useful for diagnosing or treating autoimmune diseases, e.g. rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.0%; Score 122; DB 13; Length 321019; 76.8%; Pred. No. 4.2e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 16; SEQ ID NO 1664; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alexander HC;
                                                                                                         ADS36450 standard; DNA; 321019 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAR-2003; 2003US-0455444P.
25-APR-2003; 2003US-0465241P.
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                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Begovich AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-728480/71.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004083403-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cargill M,
                                                                                                                                                                                                                               16-DEC-2004
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                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polymucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for
                                                                                                                                                                                                                                                                              CGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTCTTACATCTTCAAGTGCTAGAAATG 181
CA gene in a cell. The composition and methods are useful for detecting, diagnosing, preventing and treating cancers, especially lymphoma and leukaemia. These may also be used in screening for agents that modulate cancer. The present sequence is a human CAP genomic sequence. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                  Sequence 329019 BP; 84190 A; 70461 C; 76072 G; 98276 T; 0 U; 20 Other;
                                                                                                                                                                                                                             CGAACTTCAAACCTCAGGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTAGGATTACAGG
                                                                                                                                                                            CCGGCTAATTTTGTATCTTTAGTAGAGGCGCGTTCCTCCATGTTGGTCAGGCTGGTCT
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing
                                                                                                                                                     ;
0
                                                                                                                            Length 329019;
                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ovarian cancer; ovarian tumour; cytostatic; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ovarian cancer related cDNA clone SEQ ID NO:6944.
                                                                                                                                                     0; Mismatches 45;
                                                                                                                          , DB 13;
4.2e-17;
                                                                                                                           Score 122;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 6944; 489pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones
                                                                                                                                                                                                                                                                                                                                                                                                                    ABL83966 standard; cDNA; 381 BP
                                                                                                                                                                                                                                                                                                                                                       171456 AATATGAAAGCAAA 171443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-2000; 2000US-0207484P
                                                                                                                            34.0%;
76.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-2001; 2001WO-US017756
                                                                                                                                                                                                                                                                                                                               182 CTTATGAAAACGAA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harlocker SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                     Matches 149; Conservative
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                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide
                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                               122
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detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (II). (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 TCGAACTCCTGACCTCAGGTGATCCACCCGCCTCGGCCTTCCAAAGTGCTGGGATTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deigner H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cccaectaatrititgractritiagiagagacgaggriticgccaigritiggccaggctiggic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGAACTTCAAACCTCAGGTGATCCGCCCCGCCTCGGCCTCCCAAAGTGCTAGGATTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCGGCTAATTTTGTATCTTTTAGTAGACGCCGTTCCTCCATGTTGGTCAGGCTGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zipfel PF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 381 BP; 115 A; 83 C; 91 G; 92 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human SIRS/sepsis diagnostic marker DNA fragment 10381.
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0; Mismatches 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 121.8;
Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                       library using well known techniques
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08-AUG-2003; 2003DE-01036511.
02-SEP-2003; 2003DE-01040395.
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77.8%;
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Matches 147; Conservative
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The invention relates to a novel method for in vitro detection of systemic inflammatory response syndrome (SIRS). The method comprises detecting abnormal expression of disease-related genes, or their associated peptides. The method of the invention demonstrates antibacterial, immunosuppressive and antiinflammatory applications and may be used for early differential diagnosis, monitoring progression, espessing risk, assessing the likely response to treatment and for post mortem diagnosis of systemic inflammatory response syndrome, sepsis and sepsis-like conditions. The recombinant or synthetic nucleic acid sequences of the invention, or derived proteins or peptides, may be useful as calibrants in assays for the specified diseases, for evaluating activity or toxicity in screening for active agents and/or for activity or toxicity in screening for active agents and/or for cativity or toxicity in screening for active agents and/or for cativity or toxicity in screening for active agents and/or for evaluating preparation of agents for treatment or prevention of the specified diseases. The current sequence is that of a human SIRS/sepsis diagnostic marker DNA fragment of the invention. Note: The sequence data for this cateronic format directly from WIPO at ftp. vipo.int/pub/published control format directly from WIPO at ftp. vipo.int/pub/published control format directly from WIPO at ftp. vipo.int/pub/published control format directly from WIPO at proper and publication and formating indexing due to inconsistencies in application and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 546 BP; 180 A; 125 C; 122 G; 117 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding novel human diagnostic protein #26780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 33.9%; Score 121.8; DB 1:
Local Similarity 77.8%; Pred. No. 1.4e-17;
Les 147; Conservative 0; Mismatches 42
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23-AUG-2000; 2000US-00649167
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Matches
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain careaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed continuous. (I) is useful in gene therapy techniques to restore normal custul for generating antibodies against it, detecting or quantitating a polymeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders in colympetide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cand to produce other types of data and products dependent on DNA and mino acid sequences of the invention. Note: The sequence data for this partners in the printed specification, but was obtained in
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                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 556 BP; 177 A; 129 C; 124 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                     Claim 1; SEQ ID NO 26780; 103pp; English
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                                              P-PSDB; ABG26789
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yz51e02.81 9 EA25 Subt 170004241

N67313 yz: BU198009 I CN415426 BM995211

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Contact: Genoscope
Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
Z rue Gastono Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a Noti-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCWWSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL520459 1071 bp mRNA linear EST 24-MAR-2004
AL520459 Homo sapiens NETROBLASTOMA COT 10-NORMALIZED Homo sapiens
CDNA clone CSODB006YA12 3-PRIME, mRNA sequence.
AL520459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mgNa"
/db_xref="taxon:9606"
/clone="CsObboOsYAl2"
/tissue type="mUROBLASTOWA COT 10-NORMALIZED"
/clone_Tib="Homo sapiens NEUROBLASTOWA COT 10-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ScoR v sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        For more information about this cluster, see http://www.genoscope.cns.fr/cdna?8=CS0DB006BA06NP1&c=6092.r. Location/Qualifiers
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1 (bases 1 to 1071)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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BX505458
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AA126814
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AUTHORS
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CR60908 full-leng
CR926093 bongo pyg
AA678616 ah03c11.9
T96411 ye34e04.81
AQ419825 RFCI-11-1
AA368329 EST79571
CR823193 ij25f02.y
AW071821 xa99h09.x
AW390284 CM2-ST018
CB06875 is30a03.x
AA644223 ab63e10.8
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AA64426 nac30h01.
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AM440568 xt15e04.x
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nd18f02.s
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                                                                                                                                                                                                                                                                  cccggctaattttgtatctt......ttttttatagtgttctggaa 359
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                         5.1.8
Biocceleration Ltd.
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                         version :
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
                       GenCore (c) 1993
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121.8
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Perfect score:
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EST 24-MAR-2004

34.7%; Score 124.4; DB 1; Length 1071;

Query Match

nac30h01. ij25f02.y xt15e04.x 601433420

ah08g03.s

AA678932

tal3c04.x

AA581498 A1472736 BF475466

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AA644223

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Result No.

121.

BQ101225 AW440568 BE892611 AA678932

A1889955 wm80c03.x BQ778458 i131d07.x BX505458 BYE2D686E AA126814 zn87210.r CA420015 UI-H-FH0-CD246087 AGENCOURT CD34665 UI-H-FP2-CN263776 170004241 CA442904 UI-H-DP0-CR867781 Pongo pyg CR867781 Pongo pyg GR867181 Pongo pyg BM997829 UI-H-DI0-AQ559212 HS 2069 B BM997829 UI-H-DI0-AQ5644586 M85a05.x CN264773 170004245 BF931566 IL2-NT020

Scoring table:

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Database

Searched:

UI-H-EDO-wm80c03.x il31d07.x DKFZp686E zn87c10.r UI-H-FHO-

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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         скузбо93 2825 bp mRNA linear HTC 06-DEC-2004
Pongo pygmaeus mRNA; cDNA DKFZp45902210 (from clone DKFZp45902210).
CR926093
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                                                                          21-JUL-2004
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1 (bases 1 to 2825)
Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pongo pygmaeus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                 CR609780 1755 bp mRNA linear HTC Chill-length cDNA clone CS0D8006YA12 of Neuroblastoma Cot Cormalized of Homo sapiens (human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db xref="taxon:9606"
/clone="cSobBooksA12"
/plasmid="ppe="Neuroblastoma Cot 10-normalized"
/plasmid="ppe="Neuroblastoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1755;
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1 (bases 1 to 1755)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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Pred. No. 8.2e-13;
0; Mismatches 21;
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HTC; CNSLT_CDNA.
Homo sapiens (human)
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Matches 137; Conservative
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full-length cDNA clone CS0DF033Y108 of Fetal brain of Homo sapiens
(human).
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                                                                                                                   TCGAACTTCAAACCTCAGGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTAGGATTACAG 120
                                                                                                                                                                                                                                      252 TCGAACTCCTGACCTCATGTGATCCGCCCCCCTCGGCTTCCCAAGTGCTGGGATTACAG 193
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                     CCCGCCTAATTTTGTATCTTTAGTAGAGGCGGCGTTCCTCCATGTTGGTCAGGCTGGTC
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http://fulllength.invitrogen.com/ invitroGen Corporation 1600
Faraday Avenue
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1. (bases 1 to 1686)
Li W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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  Pred. No. 8.9e-13;
0; Mismatches 21;
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/plasmid="pCMVSPORT_6"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODF033YI08"
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1. .1686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CR619941.1 GI:50500748
HTC; CNSLT_cDNA.
Homo sapiens (human)
86.78;
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  Best Local Similarity 86.7
Matches 137; Conservative
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/dex="pooled (6)"
/lab host="DH10B"
/lab host="DH10B"
/lab host="DH10B"
/clone_lib="Gesaler Wilms tumor"
/clone_lib="Gesaler Wilms tumor"
/note="Vector: pSPRRT1; Site 1: Sal1; Site_2: NotI; RNA
was prepared from a pool of anonymous Wilms' tumor RNAs.
RNA was prepared by acid-phenol, followed by one round of
oligo dT selection. CDNA library preparation was with
the BRL/Life Tech. Superscript Plasmid System. An
oligo-dT NotI primer for first strand synthesis generated
gcggccgcc(c(t) n at the 3' end of the clones. A 5' Sal1
adaptor was used with sequence 5'-gtcgaccacgctccg-3'.
Resulting CDNAs were aize selected (average size 2 kb),
NotI digested, and ligated into NotI/Sal1-cut pSPORT1.
Library was constructed by Dr. Manfred Gessler."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TCGAACTICAAACCICAGGIGAICCGCCCGCCTCGGCCTCCCAAAGIGCTAGGATTACAG 120
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ah03c11.81 Gessler Wilms tumor Homo sapiens cDNA clone
IMAGE:1155572 3' similar to contains Alu repetitive element;, mRNA
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                       Hominidae, Homo.

I (bases 1 to 206)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., WashU-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
441 Ed. 134 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 206.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:1155572"
                                                                                                                                                 AA678616.1 GI:2659138
EST.
                                                                                                                                                                                                                         Homo sapiens (human)
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/mol type="mRNA"
/db xref=taxon:9600"
/clone="brackground:"
/clone lib="459 (synonym: pcorl). Vector pSportl_Sfi; host DH10B; FillA + SfilB + SfilB + SfilA + SfilB + Monday + Stage="adult"
/note="Gamma-tubulin complex component 4 (Homo sapiens),
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                                                                                                                                     Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Gesearch Center (DKPZ); Email s. wiemannoditz-heidelberg.de;
sequenced by Agowa (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKPZp45902210) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
Please contact RZPD for ordering:
Phttp://www.rzpd.de/cgj.bin/products/cl.cgj?CloneID=DKFZp45902210
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
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           Fobo,G., Han,M. and Wiemann,S.
The German cDNA Consortium
Direct Submission
Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
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protein id="CAI29719.1"
db_xref="G1:56403868"
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/codon_start=1
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AA678616

RESULT 5 AA678616/c LOCUS

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AA368329 20.2 bp mRNA linear EST 21-APR-1997 EST79571 Placenta I Homo sapiens cDNA similar to EST containing Alu AA368329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seg primer: SP6 Class: BAC ends.
                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 624)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
                                                                                                                                                                                                                                                                                                         Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Lymphocytes"
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/noce="Vector: pBAce3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 ccescraarrirrenarrirragradadaredagirrescearerresceaescraerer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
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0
RPCI-11-179F14.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-179F14, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
Other GSSs: RPCI-11-179F14.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
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75.4%; Pred. No. 1.8e-12;
tive 0; Mismatches 50;
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/organism="Homo sapiens"
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/db_xref="GDB:7568485"
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clone="RPCI-11-179F14"
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                                                                         AQ419825.1 GI:4477549
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                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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AA368329/c
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/lab host="SOLR cells (kanamycin resistant)"
/lab host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene lung (#937210)"
/note="Organ: lung; Vector: pBluescript SK-; Site 1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Dijgo dr. normal lung. Average insert size: 1.0 kb;
Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAMTTGGGARGAGGG
3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTTTTTTTTT 3'"
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       EST 27-MAR-1995
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                                                                                                                                                                                                                                                                                                         Hillier, L., Lenon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hulman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Le, Morce, B., Mortis, M., Parsons, J., Parange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                             re34e04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE:119646 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                   Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata, Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stops: 305
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (Info@image:llnl.gov) for further information.
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0
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 410;
       linear
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34.3%; Score 123; DB 8;
Best Local Similarity 92.8%; Pred. No. 1.9e-12;
Matches 129; Conservative 0; Mismatches 10;
       mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/db_xref="GDB:487935"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: -21m13
High quality sequence stop: 305.
Location/Qualifiers
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       410 bp
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                                                                                                                                                                        sapiens (human)
                                                                                                                         F96411.1 GI:735035
                                                                                                                                                                                                                                                                    Hominidae; Homo.
1 (bases 1 to 410)
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                                                                                                                                                                                                Homo sapiens
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AQ419825
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/tissue type="Islets of Langerhans"
/dev_stage="Adult"
/dev_stage="Adult"
/lab_hote:"Malton Normalized Human Islet 4 N4-HIS 1"
/clone lib="Melton Normalized Human Islet 4 N4-HIS 1"
/clone lib="Melton Normalized Fortility Site_1: Not 1;
Site_2: Sal 1; Starting 1ibrary constructed using
SuperScript Plasmid Library kit (Life Technologies) cDNA
made by oligo-dr priming. Size-selected by column
fractionation, average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
zo. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 CCCAGCTAATTTTTTTTTTTAGTAGACGAGGTTTCGCCATGTTGGCCAGCTGGTC 117
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                                                                                                                                                                                                                                                                   This read has been verified (found to hit its original self in the
                                                                                                                                                                                                 Email: dmelton@biohp.harvard.edu
This read is a 5' RESEQUENCE of a previously sequenced pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCGGCTAATTTTGTATCTTTAGTAGAGGCGCGTTCCTCCATGTTGGTCAGGCTGGTC
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WashU-Harvard Pancreas EST Project
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6135699"
                                                                                                                                                                                                                                                                                               correct orientation)
Seg primer: -40RP from Gibco.
Location/Qualifiers
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AW078821.1 GI:6033973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Both"
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                                                                                                                                                         Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                   γ. .350
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Melton,D., Marra,M., Pape,D.,
Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B.,
Rylie,T., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,
McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and
Bowers,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

For clone availability, additional sequence and expression

information related to this BST, please check the TIGR Human Gene

Index (http://www.tigr.org/tdb/hgi/hgi.html)

Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
//organism="Homo sapiens"
//mol type="mRNA"
//db_xref="ArtCC (inhost):173016"
//db_xref="type="placenta"
//db_xref="type="placenta"
//dow_stage="fetus"
//clone lib="Placenta I"
//note="forgan: placenta, Vector: pBluescript SK-; Site_1:
ECORI; Site_2: ECORI"
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
                                                                                                                                                                                     Venter, J.C.
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                          Hominidae, Homo.

1 (bases 1 to 202)
Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.1%; Score 122.4; DB 1; Length 202; 86.5%; Pred. No. 2.8e-12;
                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850 USA
713 3018699056
Fax: 3018699423
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Bioinformatics
         AA368329.1 GI:2020648
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Homo sapiens
                                                   sapiens (human)
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Matches 135; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="INAGE:2574977"
/tissue_type="juvenile granulosa tumor"
/lab.host="DH10B"
/clone lib="NCI CGAP_CO17"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: NOt1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."
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1 (Dases 1 to 355)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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      Homo aspiens
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Mammalia; Eutheria; Euarchontoglires; Primetes; Catarrhini;
                                                                                            Hominidae, Homo.
1 (bases 1 to 2)
NCI-CBASES 1 to 2)
NCI-CBASE 1 to 2)/www.ncbi.nlm.nih.gov/ncicgap.
NCI-CBAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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ilarity 77.8%; Pred. No. 3.2e-12;
Conservative 0; Mismatches 42;
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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/wol type="manna"
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/wol type="manna"
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/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
image.llnl.gov/image/hml/iresources.shtml
Seq primer: -400P from Gibco.
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mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCGGCTAATTTTGTATCTTTTAGTAGACGCGTTCCTCCATGTTGGTCAGGCTGGTC
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HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGACATCAA 140
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Best Local Similarity
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_l:
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_l:
Not1; Site_2: XhoI; cDNA made by oligo-dT priming.
Size=selected on agarose gel. Average insert size -lkb. 5.
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permute Lab), Washington University
School of Medicine, Box 8127, 660 South Brolid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TCGAACTTCAAACCTCAGGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTAGGATTACAG 120
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 348.
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1 (bases 1 to 366)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                             1. .364

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/tissue type="Purified pancreatic islet"

/lab_hogt="DH10B"
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Unpublished (1997)
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AI347665/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: stomach; Vector: puc18; Site_1: Smal; Site_2: Smal; A min1-library was made by Croning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o;
                This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-ST0182-221099-023-f05&t3=1999-10-22&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGAACTTCAAACCTCAGGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTAGGATTACAG 120
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 cccaecraarrirrgracrirriagradadadegaggrircgccargriggccaggcriggrc 121
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Unpublished (2000)
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0
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Pred. No. 3.2e-12;
0; Mismatches 42
                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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                                                                                                                                                                             Seg primer: puc 18 forward
High quality sequence stop: 363.
Location/Qualifiers
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Best Local Similarity 77.8%;
Matches 147; Conservative (
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1 (bases 1 to 364)
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Fax: 617-495-8557
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CB068575
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                                                                                                                                                                                                                                                                                                                                                                  double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ab63e10.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:845514 3' similar to contains Alu repetitive element;, mENA
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 376)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Tan,F., Wathe,Y., Wylie,T., Waterston,R. and Wilson,R. Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCGGCTAATTTTGTATCTTTAGTAGACGCCGTTCCTCCATGTTGGTCAGGCTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                             tissue type="2 pooled tumors (clear cell type)" /lab_hogt="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 366;
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found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 436 Std Brror: 0.00
Seq primer: -400P from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.9%; Score 121.8; DB 1; Best Local Similarity 77.8%; Pred. No. 3.2e-12; Matches 147; Conservative 0; Mismatches 42;
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                                                                                                                                'organism="Homo sapiens"
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                                                                                                                                                                                                  'clone="IMAGE:1916746"
                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
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AA644223.1 GI:2569441
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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_tref="uaxon:9606"
/clone="IMAGE:845514"
/tissue_type="lung carcinoma"
/cell_line="MCI-H69"
/dev_gtage="cell_line NCI-H69"
/dav_gtage="cell_line NCI-H69"
/dav_gtage="cell_line NCI-H69"
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/dov_gtage="cell_line NCI-H69"
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IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 534 Std Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham. Location/Qualifiers
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Pred. No. 3.2e-12;
0; Mismatches 42
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77.8%;
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Best Local Similarity 77.8
Matches 147; Conservative
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Job time : 2657 secs
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| cgn2_6/ptodata/1/ina/1_COMB.seq:*
| cgn2_6/ptodata/1/ina/5_COMB.seq:*
| cgn2_6/ptodata/1/ina/6A_COMB.seq:*
| cgn2_6/ptodata/1/ina/6B_COMB.seq:*
| cgn2_6/ptodata/1/ina/H_COMB.seq:*
| cgn2_6/ptodata/1/ina/PP_COMB.seq:*
| cgn2_6/ptodata/1/ina/PP_COMB.seq:*
| cgn2_6/ptodata/1/ina/PP_COMB.seq:*
| cgn2_6/ptodata/1/ina/PP_COMB.seq:*
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US-09-949-016-25489

US-09-949-016-25490

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| Sequence 1450.24|
| Sequence 1450.25|
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WIMBER: US/09/949,016 |
| CURRENT APPLICATION NUMBER: US/09/949,016 |
| CURRENT FILING DATE: 2000-04-14 |
| PRIOR FILING DATE: 2000-10-20 |
| PRIOR FILING DATE: 2000-10-30 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-06 |
| NUMBER OF SEQ ID NOS: 207012 |
| SOFTHAME: PRESESE FREESEQ for Windows Version 4.0 |
| SEQ ID NO 14502 |
| LENGTH: 18346
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Pred. No. 1.6e-21;
0; Mismatches 27; Indels
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US-09-949-016-16717
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US-09-949-016-14592
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OTHER INFORMATION: n = A,T,C or .
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Matches 140; Conservative
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  Sequence 13173, Application US/09949016

| Sequence 13173, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| FILE REFRENCE: CLOU3.07 |
| CURRENT APPLICATION NUMBER: US/09/949,016 |
| CURRENT PILING DATE: 2000-04-14 |
| PRIOR APPLICATION NUMBER: 60/231,768 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SEQ ID NO 13173 |
| LENGTH: 360470 |
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17457
LENGTH: 41182
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OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 69.69
Matches 167; Conservative
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ORGANISM: Human
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US-09-949-016-13173
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: AND USES THEREOF

TITLE OF INVENTION: AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,002

CURRENT APPLICATION NUMBER: 60/231,401

PRIOR APPLICATION NUMBER: 60/231,401

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEC ID NOS: 10823

SOFTWARE: FRAESEQ FOR WINDOWS Version 4.0
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     Length 41182;
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                                                52;
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       DB 3;
Score 122.8; DB Pred. No. 3e-21; 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                     16598 CCTGTCAAAGAAGACAATAACCAAT 16573
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US-09-99-016-14759/c
; Sequence 14759, Application US/09949016
; Patent No. 6812339
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; Patent No. 6900016
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US-09-949-002-785
     34.2%;
74.8%;
                            Best Local Similarity 74.8
Matches 154; Conservative
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Best Local Similarity
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US-09-949-002-785/c
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ORGANISM: Human
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USOUR APPLICATION US/09949016

Sequence 25499, Application US/09949016

Sequence 25499, Application US/09949016

Sequence 25499, Application US/09949016

PATENTIANIE USOURATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WIMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

SEQ ID NO S-5489

LENGTH: 601

LENGTH: 601
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19-09-949-016-25490/c

19 Gequence 25490, Application US/09949016

19 Patent No. 681239

19 GENERAL INFORMATION:

1 TITLE OF INVENTION: DOLYMORPHISMS IN KNOWN GENES ASSOCIATED

1 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 TITLE OF INVENTION: WINH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 TITLE OF INVENTION: WINHER: US/09/949,016

1 CURRENT FILING DATE: 2000-04-14

1 PRIOR APPLICATION NUMBER: 60/241,755

1 PRIOR APPLICATION NUMBER: 60/241,756

2 PRIOR PELING DATE: 2000-10-20

3 PRIOR PILING DATE: 2000-10-03

4 PRIOR PILING DATE: 2000-10-03

5 PRIOR PILING DATE: 2000-10-03

6 NUMBER OF SEQ ID NOS: 207012

6 SEQ ID NOS: 207012

7 SEQ ID NO 25490
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424 ITGAACTCCTGACCTCAGGTGATCTGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAG 365
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Pred. No. 1.3e-21;
0; Mismatches 25; Indels
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                                                                                              364 GCGTGAGCCACCGCCCGGCCAGTTTTTACTTTTTCTAAAA 323
                                                                 121 GCGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTCTTACA
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Best Local Similarity 84.6
Matches 137; Conservative
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; ORGANISM: Human
US-09-949-016-25489
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; ORGANISM: Human
US-09-949-016-25490
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; Sequence 25488, Application US/09949016
; Patent No. 6812339
; GENBEAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    FILE REPRENCE: CLOO1307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT APPLICATION NUMBER: 60/241,755
    PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFFTARE: FEBLEEC for Windows Version 4.0
                          APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 14759

LENGTH: 31618
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Pred. No. 1.3e-21;
0; Mismatches 25; Indels
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Pred. No. 3.9e-21;
0; Mismatches 28;
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84.6%;
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Best Local Similarity 83.8%;
Matches 150; Conservative
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Best Local Similarity 84.6'
Matches 137; Conservative
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ORGANISM: Human
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US-09-949-016-14759
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; ORGANISM: Human
US-09-949-016-73667
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US-09-949-016-73666
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| Sequence 25491, Application US/09949016
| Sequence 25491, Application US/09949016
| Sequence 25491, Application US/09949016
| Sequence 25491, Application US/0949016
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craiq et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| CURRENT PELICATION NUMBER: US/09/949,016
| CURRENT FILING DATE: 2000-04-14 |
| PRIOR FILING DATE: 2000-10-20 |
| PRIOR PELICATION NUMBER: G0/231,768 |
| PRIOR PELICATION NUMBER: G0/231,498 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SOFTHARE: BastSEQ for Windows Version 4.0
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERBNCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
FURE REFERBNCE: CLO01307
CURRENT PLING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
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                                                                                         1 CCCGGCTAATTTTGTATCTTTTAGTAGAGACGCGTTCCTCCATGTTGGTCAGGCTGGTC
                                            Gaps
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Score 122; DB 3; Length 601;
Pred. No. 1.3e-21;
0; Mismatches 25; Indels
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34.0%; Score 122; DB 3; Length 601;
Best Local Similarity 84.6%; Pred. No. 1.3e-21;
Matches 137; Conservative 0; Mismatches 25; Indels
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    Query Match
Best Local Similarity 84.6%;
Matches 137; Conservative 0
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US-09-949-016-73666/c
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LENGTH: 601
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Sequence 73667, Application US/09949016

Sequence 73667, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

TENTING 10 73667
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84.6%; Pred. No. 1.3e-21;
ative 0; Mismatches 25;
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Pred. No. 1.3e-21;
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84.6%; Pred. No. 1...
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 73666
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Best Local Similarity 84.67
Matches 137; Conservative
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Matches 137; Conservative
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US-09-949-016-73668/c
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25; Indels
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Pred. No. 4.7e-21;
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13886
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Best Local Similarity 84.6%;
Matches 137; Conservative
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; Sequence 73669, Application US/09949016
; Betten No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT PILING DATE: 2000-010-20
; PRIOR PILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWAMER: PRESEC FOR Windows Version 4.0
Sequence 73668, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: 60/29,016
CURRENT FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTHAND APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 73668
LENGTH: 601
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Pred. No. 1.3e-21;
0; Mismatches 25; Indels
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Pred. No. 1.3e-21;
0; Mismatches 25; Indels
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Best Local Similarity 84.6
Matches 137; Conservative
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Best Local Similarity 84.6
Matches 137; Conservative
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US-09-949-016-73668
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Sequence 12122, Application US/09949016
| Saguence 12122, Application US/09949016
| Patent No. 6812339
| GENERAL INPORMATION:
| APPLICANT: VEWTER, J. Craig et al. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| FILE REPRENCE: CL001307 |
| CURRENT APPLICATION NUMBER: US/09/949,016 |
| CURRENT FILING DATE: 2000-04-14 |
| PRIOR FILING DATE: 2000-10-20 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                            RESULT 14

US-09-949-016-13886/c

j Sequent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRESENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

FRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

FRIOR PILING DATE: 2000-10-03
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1: /cgn2_6/ptodata/1/pubpna/USO3_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

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SUMMARIES

	Description	Sequence 5, Appli	Sequence 72033, A	Sequence 72034, A	Sequence 72035, A	Sequence 13830, A	Sequence 117277,	Sequence 117278,	Sequence 117277,	Sequence 117278,	Sequence 44, Appl	Sequence 35, Appl	Sequence 591033,	Sequence 724096,	Sequence 17566, A	Sequence 48, Appl	Sequence 6944, Ap	Sequence 47240, A	Sequence 33, Appl	Sequence 26780, A	Sequence 25055, A	Sequence 33, Appl	Sequence 33, Appl	Sequence 684936,
	ΩI	US-10-009-579-5	US-09-925-065A-72033	US-09-925-065A-72034	US-09-925-065A-72035	US-10-357-930-13830	US-10-027-632-117277	US-10-027-632-117278	US-10-027-632-117277	US-10-027-632-117278	US-10-417-375-44	US-10-235-192A-35	US-09-925-065A-591033	US-09-925-065A-724096	US-10-741-600-17566	US-10-388-838-48	US-09-867-701-6944	US-09-925-065A-47240	US-10-933-118-33	US-10-450-763-26780	US-10-357-930-25055	US-10-737-082-33	US-10-765-790-33	US-09-925-065A-684936
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	Score	359	124	124	124	123.8	123.6	123.6	123.6	123.6	123	122.4	122	122	122	122	121.8	121.8	121.8	121.8	121.8	121.8	121.8	121.6
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Sequence 684938,	Sequence 267232,	Sequence 267232,	Sequence 6848, Ap	Sequence 17759, A	Sequence 226, App	Sequence 4, Appli	Sequence 4, Appli	Sequence 15, Appl	Seguence 684937,	Sequence 709882,	Sequence 709883,	Sequence 704720,	Sequence 26761, A	Sequence 26761, A	Sequence 191, App	Sequence 191, App		Sequence 88, Appl	Seguence 563601,	Sequence 244, App	Seguence 933530,
US-09-925-065A-684938	US-10-027-632-267232	US-10-027-632-267232	US-10-719-993-6848	US-10-741-600-17759	US-10-085-117-226	US-10-115-278-4	US-10-762-966-4	US-10-229-058B-15	US-09-925-065A-684937	US-09-925-065A-709882	US-09-925-065A-709883	US-09-925-065A-704720	US-10-027-632-26761	US-10-027-632-26761	US-09-764-855-191	US-10-072-349-191	US-10-737-082-88	US-10-765-790-88	US-09-925-065A-563601	US-10-085-117-244	US-09-925-065A-933530
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121.6	121.6	121.6	121.4	121.4	121.4	121.2	121.2	121.2	121.2	121.2	121.2	120.8	120.8	120.8	120.8	120.8	120.8	120.8	120.4	120.4	120.2
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GREARAL INFORMATION:
GREARAL INFORMATION:
APPLICANT: Ruiters, Marcel H.J.
APPLICANT: Ruiters, Marcel H.J.
APPLICANT: McLaughlin, Pamela M.J.
APPLICANT: Harmsen, Martin C.
APPLICANT: Harmsen, Martin C.
APPLICANT: Terpstra, Peter
APPLICANT: Terpstra, Peter
APPLICANT: Non-squamous epithelium-specific transcription
FILE REFERENCE: P52075US00
CURRENT APPLICATION NUMBER: US/10/009,579
CURRENT FILING DATE: 2000-03-01
FRIOR APPLICATION NUMBER: EP 00200728.4
FRIOR APPLICATION NUMBER: PCT/NL01/00166
FRIOR PRILING DATE: 2001-03-28
FRIOR FILING DATE: 2001-03-28
SOFTWARE: PETENTON NUMBER: PCT/NL01/00166
FRIOR FILING DATE: 2001-02-28
SOFTWARE: PATENTON NUMBER: PCT/NL01/00166
FRIOR FILING DATE: 2001-02-28
SOFTWARE: PATENTON NUMBER: PCT/NL01/00166
FRIOR FILING DATE: 2001-02-28
SOFTWARE: PATENTON NUMBER: PA
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; CTHER INFORMATION: /note="EGP-2 promotor sequence from -3967 to +315"
US-10-009-579-5
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Sequence 5, Application US/10009579; Publication No. US20020156041A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 359; Conservative
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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                                                                                                             GCTTATGAAAACGAAAAAAAATTATTAAGAGTAATTATAAAGAAACACTCATTTTCTTC
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US-09-925-065A-72033/C

Sequence 72033, Application US/09925065A

Publication No. US20050228172A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Uncleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR PILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR PAPLICATION NUMBER: US 60/252,147

PRIOR PELING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR PELING DATE
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Matches 184; Conservative
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ORGANISM: Homo sapiens
US-09-925-065A-72033
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RESULT 3 US-09-925-065A-72034/c ; Sequence 72034, Application US/09925065A ; Publication No. US20050228172A9

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1159 GCGTGACCCACCGCCCCCCCCCCCCCTTTTTCCATATTACAATATGAACAATTA 1100
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Sequence 72035, Application US/09925065A

Publication No. US20050228172A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome

TITLE OF INVENTION: NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR PILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-01-16

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: PASTESEQ for Windows Version 4.0
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PILING DATE: 2000-10-24
PRIOR PLLING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-01-16
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Pred. No. 2.1e-19;
0; Mismatches 100;
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Matches 184; Conservative
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109 CCGGCTAATTTTTGTATTTTAGTAGAGGTTTTCACCATGTTGGCCAGGCTGATCT 168
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 117277
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Best Local Similarity 64.4%;
Matches 183; Conservative
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US-10-027-632-117277
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APPLICANT: Schlegel. Robert
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Monaban, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR PLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR PLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR PLING DATE: 2000-06-09
PRIOR PLING DATE: 2000-06-09
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ 1D NOS: 62232
NUMBER OF SEQ 1D NOS: 62232
PRIOR FILING DATE: 2000-12-13
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                                                                                                                           Length 2041;
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Pred. No. 2.1e-19;
0; Mismatches 100; Indels
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                                                                                                                               Query Match
Best Local Similarity 64.8%;
Matches 184; Conservative
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Best Local Similarity 68.8
Matches 170; Conservative
    ; SEQ ID NO 72035
; LENGTH: 2041
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-72035
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LENGTH: 438
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                                                                                                            CGTGAGCCACCGCGCTCAGCCTGGGAACACCCTTTTCTTACATCTTCAAGTGCTAGAAATG 181
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RESULT 6

US-10-027-632-117277/c

§ Sequence 117277, Application US/10027632

§ Sequence 117277, Application US/10027632

§ Sequence 117277, Application US/10027632

§ Publication No. US20020198371A1

§ GENERAL INFORMATION:

† TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

† TITLE OF INVENTION: Polymorphisms in the Human Genome

† TITLE OF INVENTION: Polymorphisms in the Human Genome

† FILE REFERENCE: 108827, 129

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-03-20

PRIOR FILING DATE: 2000-03-20

PRIOR PILING DATE: 2000-03-29

PRIOR PELING DATE: 2000-03-29

PRIOR PELING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28
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Pred. No. 2e-19;
1; Mismatches 100; Indels
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 1000-03-24
PRIOR PILING DATE: 1000-03-24
PRIOR PILING DATE: 1099-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-00-28
PRIOR FILING DATE: 1999-00-38
PRIOR PILING DATE: 1999-00-38
PRIOR FILING DATE: 1999-00-38
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Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REPRENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30
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Pred. No. 2e-19;
1; Mismatches 100;
                                                                                                                                  5-10-027-632-117278/c
Sequence 117278, Application US/10027632
Publication No. US20020198371A1
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Best Local Similarity 64.4%;
Matches 183; Conservative
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US-10-027-632-117277/c
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Sequence 117278, Application US/10027632

Publication No. US2003020407549

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: POLYMorphisms in the Human Genome

TILE OF INVENTION: 10827-129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 1909-01-32

PRIOR PLING DATE: 1909-01-32

PRIOR PLING DATE: 1909-01-32

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-01-28

PRIOR PLING DATE: 1999-09-28

PRIOR PLING DATE: 1999-09-28

PRIOR PLING DATE: 1999-09-28

PRIOR PLING DATE: 1999-09-09

PRIOR PLING DATE: 1999-09-09

PRIOR PLING DATE: 1999-09-09

PRIOR PLING DATE: 1999-09-09
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Pred. No. 2e-19;
1; Mismatches 100; Indels
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
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Best Local Similarity 64.4%
Matches 183; Conservative
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US-10-027-632-117278/c
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US-10-027-632-117277
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                                                                                                                         Length 1136;
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Pred. No. 1.4e-18;
0; Mismatches 50; Indels 0
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US-10-417-375-44/c

Sequence 44, Application US/10417375

Publication No. US20040219528A1

GENERAL INPORMATION:

APPLICANT: David W. Morris

APPLICANT: Marc Malandro

TITLE OF INVENTION: Novel Therapeutic Targets in Cancer;

FILE REFERENCE: 529452001600

CURRENT APPLICATION NUMBER: US/10/417,375

CURRENT FILING DATE: 2003-04-15

NUMBER OF SEQ ID NOS: 176

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 44

LENTH: 53623
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Pred. No. 2e-19;
1; Mismatches 100;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 117278
LENGTH: 1136
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Best Local Similarity 75.4%;
Matches 153; Conservative (
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Best Local Similarity 64.4%;
Matches 183; Conservative
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US-10-417-375-44
                                                                       ORGANISM: Human
US-10-027-632-117278
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                                                                                                                                                                                                                     Score 122.4; DB 7;
Pred. No. 3e-18;
0; Mismatches 36;
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68.6%; Pred. No. 3.3e-19;
tive 1; Mismatches 81;
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LOCATION: 151844-151943, 154924-155023
CTHER INFORMATION: N = any nucleotide
US-10-235-192A-35
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Best Local Similarity 80.0%;
Matches 144; Conservative
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Best Local Similarity 68.6
Matches 181; Conservative
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CRGANISM: Homo sapiens
US-09-925-065A-591033
                                                                                                                                                      ORGANISM: Homo sapiens
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SEQ ID NO 48
LENGTH: 329019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518 ATTITIGCIGGITAAAATAAATAAGACAGIGCIGTICIATIGAGCATTICAAATGIATC 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 ccceecnaariringraririnagradadanecacirircrecareridereadecreere 397
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                                                                                                                                                                                                        60 TGAACTCCCAACCTCAGGTGATCCGCCCCCCCTCGGCCTCCCAAAGTGCTGGGATTATAGG 119
                                                                                                                                                                                                                                                                                                                                                   182 CTTATGAAAACGAAAAAGAATTATTAAGAGTAATTATAAAGAAACACTCATTTTCTTCC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 CGAACTTCAAACCTCAGGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTAGGATTACAGG 121
                                                                                                                                                                                                                                                                             122 CGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTCTTACATCTTCAAGTGCTAGAAATG 181
61
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                                           1 CCGCCTAACTITITAT-TITITAGTAGCGACAGGGTITCTCCATGTTGGTCAGGTCTCT
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US-09-925-065A-724096
i Sequence 724096, Application US/09925065A
i Publication No. US20050228172A9
i Publication No. US20050228172A9
i GENERAL INFORMATION: Lidentification and Mapping of Single
i TITLE OF INVENTION: Lidentification and Mapping of Single
i TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
i TILE REFERENCE: 108827.135
i CURRENT APPLICATION NUMBER: US 60/243,096
i PRIOR APPLICATION NUMBER: US 60/243,096
i PRIOR PILING DATE: 2000-10-24
i PRIOR PILING DATE: 2000-11-20
i PRIOR FILING DATE: 2000-11-10
i PRIOR FILING DATE: 2000-11-10
i PRIOR APPLICATION NUMBER: US 60/250,092
i PRIOR FILING DATE: 2001-01-16
i PRIOR FILING DATE: 2001-01-01-16
i PRIOR FILING DATE: 2001-01-01-01-01-01-01-01-01-
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Pred. No. 4.7e-19;
0; Mismatches 80; Indels C
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Best Local Similarity 68.0%;
Matches 170; Conservative (
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US-09-925-065A-724096
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NAME/KEY: misc_feature

1 LOCATION: (1)...(321019)

1 COCATION: (1)...(321019)

1 COCATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-741-600-17566
NS-10-741-600-17566/c

Sequence 17566, Application US/10741600

Sequence 17566, Application No. US2050026169A1

Publication No. US2050026169A1

SEGUENCE INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: MYCOARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: MYCOARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

TITLE REPERENCE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FactSEQ for Windows Version 4.0

SEQ ID NO 17566

LENGTH: 221019
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34.0%; Score 122; DB 8; Length 329019;
Best Local Similarity 76.8%; Pred. No. 5.1e-18;
Matches 149; Conservative 0; Mismatches 45; Indels 0;
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US-10-388-838-48/c
is Sequence 48, Application US/10388338
is Publication No. US20040180344A1
is GENERAL INFORMATION:
is APPLICANT: David W. Morris
is APPLICANT: Marc Malandro
is TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
is TILE REPERENCE: 529452001600
is CURRENT APPLICATION NUMBER: US/10/388,838
is CURRENT FILING DATE: 2003-03-14
is NUMBER OF SEQ ID NOS: 114
is NUMBER OF SEQ ID NOS: 114
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; OTHER INFORMATION: n = A,T,C or G
US-10-388-838-48
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May 6, 2006, 12:11:37; Search time 423 Seconds (without alignments) 3456.361 Million cell updates/sec
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| SIDSS/ptodata/1/pubpna/USOB_NEW_PUB.seq1:*
| SIDSS/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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359
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result Nej.	Score	Query Match	Query Match Length DB	DB	ID	Description
0	124	34.5	2041	7	US-09-925-065A-72033	Sequence 72033, A
0	124	34.5	2041	7	US-09-925-065A-72034	Sequence 72034, A
0	124	34.5	2041	7	US-09-925-065A-72035	Sequence 72035, A
Α.	124	34.5	2041	11	US-10-301-480-173272	Seguence 173272,
υ u	124	34.5	2041	11	US-10-301-480-173273	Sequence 173273,
0	124	34.5	2041	11	US-10-301-480-173274	Sequence 173274,
0 0	124	34.5	2041	12	US-10-301-480-786681	Sequence 786681,
, co	124	34.5	2041	12	US-10-301-480-786682	Seguence 786682,
0	124	34.5	2041	12	US-10-301-480-786683	Seguence 786683,
10	122.2	34.0	63984	17	US-11-121-086-26	Sequence 26, Appl
11	122	34.0	464	7	US-09-925-065A-591033	Sequence 591033,
12	122	34.0	1031	7	US-09-925-065A-724096	Sequence 724096,
c 13	122	34.0	321019	10	US-10-995-561-13204	Sequence 13204, A
14	121.8	33.9	424	7	US-09-925-065A-47240	Sequence 47240, A

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8478 Seguence 148478,	Sequenc	4936 Seguence 684936,	Seguence 6	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sednence 9	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence 69	Seguence	Sequence	1 Sequence	0	Sequence 1	Seguence			97 Sequence 70669	Sequence	Segmence 628
US-10-301-480-148478			US-09-925-065A-684938	•		2 US-10-301-480-1164071	US-09-925-065A-684937	US-09-925-065A-709882	US-09-925-065A-709883	US-09-925-065A-704720	US-09-925-065A-563601	US-09-925-065A-933530	1 US-10-301-480-38290	Sn	0 US-10-995-561-13491	US-09-925-065A-764373	US-09-925-065A-694967	US-09-925-065A-694968	US-09-925-065A-694969		0 US-10-995-561-13320			US-09-925-065A-104751	1 US-10-301-480-204893		US-09-925-065A-706696	US-09-925-065A-7066	SD	1 US-10-330-773-628
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33.9	33.9	33.9	33.9	33.9	33.8	33.8	33.8	33.8	33.8	33.6	33.5	33.5	33.5	33.5	33.5	33.4	33.4	33.4	33.4	33.4	33.4	33.3	33.3	33.3	33.3	33.3	33.3	33.3	33.3	33.2
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7.	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
INFORMATION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
FILE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REPERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/260,092
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FRASERQ for Windows Version 4.0
SEQ ID NO 72033
LENGTH: 2041
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               ; Sequence 72033, Application US/09925065A; Publication No. US20040181048A1; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-925-065A-72033
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Best Local Similarity
US-09-925-065A-72033/c
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                             1219 TTGAACTCCCAACCTCAGGTGATCCACCCACCTCGGCCTCCCCAAAGTGCTAGGATTACAG 1160
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                                                                                                                                                  GCGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTCTTACATCTTCAAGTGCTAGAAAT 180
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                                                                                                     121 GCGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTCTTACATCTTCAAGTGCTAGAAAT 180
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TCGAACTICAAACCICAGGIGAICCGCCCCGCCTCGGCCTCCCAAAGIGCTAGGAITACAG
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GENERAL INFORMATION:
GENERAL INFORMATION:
ITILE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT PAPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2001-00-08
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR PRILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
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Pred. No. 5.7e+03;
0; Mismatches 100; Indels
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Best Local Similarity 64.8%;
Matches 184; Conservative
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US-09-925-065A-72034/c
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RESULT 3 US-09-925-065A-72035/c

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Sequence 17327.4, Application US/10301480

Sequence 17327.4, Application Wo. US20060057564A1

GENERAL INFORMATION: US20060057564A1

GENERAL INFORMATION: Identifiction and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: in the Human Genome

TITLE OF INVENTION: in the Human Genome

TITLE OF INVENTION: in the Human Genome

FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR PILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE FRASESEQ for Windows Version 4.0

SEQ ID NO 173272

LENGTH: 2041
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                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 72035, Application US/09925065A publication No. US20040181048A1 GENERAL INFORMATION:
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Similarity 64.8%;
84; Conservative C
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US-09-925-065A-72035
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US-10-301-480-173272/c
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Best Local Simil
Matches 184; C
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US-10-301-480-173272

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Sequence 13274, Application US/10301480

Sequence 13274, Application US/10301480

Publication No. US20060057564A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: In the Human Genome

TITLE OF INVENTION: in the Human Genome

FILE REPRENCE: 108927.137

CURRENT PILING DATE: 2002-11-21

FRIOR APPLICATION NUMBER: US 10/215,598

PRIOR FILING DATE: 2001-08-09

PRIOR FILING DATE: 2001-08-09

PRIOR FILING DATE: 2001-08-09

PRIOR FILING DATE: 2001-08-06

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17374
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Sequence 786681, Application US/10301480

Publication No. US200600575441

SEQUENCE INCORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: In the Human Genome

FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT PILING DATE: 2002-11-21

FRIOR APPLICATION NUMBER: US 60/311,695

PRIOR FILING DATE: 2001-08-09

PRIOR FILING DATE: 2001-08-09

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: Fast SEQ for Windows Version 4.0

SEQ ID NO 786681

LENGTH: 2041

TUTLE OF INVENTION NUMBER: US 60/311,695

FRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SEQ ID NO 786681

LENGTH: 2041
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Pred. No. 5.7e+03;
0; Mismatches 100;
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Best Local Similarity 64.8%;
Matches 184; Conservative (
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CORGANISM: Homo sapien
US-10-301-480-786681
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US-10-301-480-173274
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Sequence 173273, Application US/10301480
Sublication No. US20060057564A1
GENERAL INFORMATION:
APPLICAMTION:
APPLICAMTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: In the Human Genome
FILE REFERENCE: 108827.137
CURRENT PELLORION NUMBER: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SCOTTAND 172732
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34.5%; Score 124; DB 11; Length 2041; 64.8%; Pred. No. 5.7e+03; ive 0; Mismatches 100; Indels 0;
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Matches 184; Conservative
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US-10-301-480-173273
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LENGTH: 2041
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US-10-301-480-786683/c
$$ Squence 786683/c$
$$ Squence 786683 Application US/10301480$
$$ Publication No. US20060057564A1$
$$ Eublication No. US20060057564A1$
$$ GENERAL INFORMATION:
$$ TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
$$ TITLE OF INVENTION: in the Human Genome TITLE OF INVENTION: in the Human Genome TITLE OF INVENTION: in the Human Genome CURRENT PILING DATE: 2002-11-21
$$ CURRENT PRILING DATE: 2002-11-21
$$ FRIOR PAPLICATION NUMBER: US 10/215,598$
$$ PRIOR PAPLICATION NUMBER: US 60/311,695$
$$ PRIOR PAPLICATION NUMBER: US 60/311,695$
$$ PRIOR PILING DATE: 2001-08-10
$$ NUMBER OF SEQ ID NOS: 1226918$
$$ SOFTWARE: FastSEQ for Windows Version 4.0
$$ SEQ ID NO 786683
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APPLICANT: POULSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFREENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/12,086
PRIOR FILING DATE: 2005-05-04
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
SEQ ID NO 26
LENGTH: 63984
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Pred. No. 5.7e+03;
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Best Local Similarity 64.8%;
Matches 184; Conservative (
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US-11-121-086-26
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TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: In the Human Genome
FILE OF INVENTION: In the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE FEAST OF Windows Version 4.0
SEQ ID NO 786682
LENGTH: 2041
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                  Score 124; DB 12; Length 2041;
Pred. No. 5.7e+03;
0; Mismatches 100; Indels 0
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                  tch 34.5%; al Similarity 64.8%; 184; Conservative (
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CORGANISM: Homo sapien
US-10-301-480-786682
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                                                      TCGAACTTCAAACCTCAGGTGATCCGCCCCGCCTCGGCCTCCCAAAGTGCTAGGATTACAG
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Sequence 591033, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR PELING DATE: 2000-11-20

PRIOR PELING DATE: 2000-11-30

PRIOR FILING DATE: 2001-11-16

PRIOR PELING DATE: 2001-01-16

PRIOR PELING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/269,846

PRIOR SEQ ID NOS: 957068

NUMBER OF SEQ ID NOS: 957068

SEQ ID NO 591033

SEQ ID NO 591033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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Pred. No. 1.7e+04;
1; Mismatches 81; Indels
                                                                                                                                                                                    20877 GGTCAGCCACCCCCCGCCT 20899
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Best Local Similarity 68.6%;
Matches 181; Conservative 1
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US-09-925-065A-591033
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US-09-925-065A-724096
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US-09-925-065A-591033
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Sequence 724096, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:

APPLICANT: Wang, David G.

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NAME/KEY: misc feature
LOCATION: (1).T.(321019)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
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US-10-995-561-13204/c

US-10-995-561-13204, Application US/10995561

; Sequence 13204, Application US/10995561

; GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE OF INVENTION:
CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE OF INVENTION:
FILE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/995, 561

; CURRENT PILLING DATE: 2004-11-24

; WUNDER OF SEQ ID NOS: 85702

; SOFTWARE: PRESENCE for Windows Version 4.0
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
FRIOR APPLICATION NUMBER: US 60/243,096
FRIOR PAPLICATION NUMBER: US 60/252,147
FRIOR PILING DATE: 2000-11-20
FRIOR APPLICATION NUMBER: US 60/250,092
FRIOR APPLICATION NUMBER: US 60/250,092
FRIOR PRILING DATE: 2000-11-16
FRIOR PELING DATE: 2001-01-16
FRIOR PELING DATE: 2001-01-16
FRIOR PELING DATE: 2001-01-16
FRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SEQ ID NOS: 957086
SEC ID NOS: 957086
SEC ID NOS: 957086
SEC ID NOS: 957086
SEC ID NOS: 957086
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Pred. No. 1e+04;
0; Mismatches 80; Indels
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68.0%;
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US-09-925-065A-724096
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LENGTH: 321019
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Best Local Simi
Matches 170;
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; Sequence 148478, Application US/10301480

; Publication No. US20060057564A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
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GENERAL INFUGRATION:

JUTLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastERQ for Windows Version 4.0
SEQ ID NO 47240
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  Pred. No. 2.1e+02;
0; Mismatches 45; Indels
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Pred. No. 1.8e+04;
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Best Local Similarity 84.9%;
Matches 135; Conservative
ilarity 76.8%;
Conservative
                                                                                                                                                                                                                                                                                                        182 CTTATGAAAACGAA 195
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US-09-925-065A-47240
  Best Local Similarity
Matches 149; Conserv
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                                                                                                                                                                                                                                                                                                                                     DB 11; Length 424;
                                                                                                                                                                                                                                                                                                                                       Score 121.8; DB 11; Length
Pred. No. 1.8e+04;
1; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGTGAGCCACCGCGCTCAGCCTGGGAACACCTTTTCTT 159
               FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT APPLICATION NUMBER: US/10/215,598
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 148478
TITLE OF INVENTION: in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6, 2006, 12:28:15
                                                                                                                                                                                                                                                                                                                                     Query Match 33.9%;
Best Local Similarity 84.9%;
Matches 135; Conservative
                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapien
US-10-301-480-148478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: May
Job time : 425 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176
                                                                                                                                                                                                                                                          TYPE: DNA
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